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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 20:27:58 ; Search time 16892 Seconds  
(without alignments)  
11573.266 Million cell updates/sec

Title: US-10-016-496-1  
Perfect score: 4134  
Sequence: 1 aattccgtgtgtcgggttc.....aagcgcccgacagcaagg 4134

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4134	100.0	4134	6	AR182343 Sequence
2	4134	100.0	4134	6	AR236221 Sequence
3	4134	100.0	4134	6	AR243543 Sequence
4	4134	100.0	4134	6	AR254415 Sequence
5	4134	100.0	4134	6	AR321738 Sequence
6	4134	100.0	4134	6	AR411424 Sequence
7	4134	100.0	4134	6	AR432994 Sequence
8	4134	100.0	4134	6	AX417770 Sequence
9	4134	100.0	4134	6	AX449101 Sequence
10	4134	100.0	4134	6	AX743965 Sequence
11	4116	99.6	4116	5	AF406649 Squalus a
12	1745.2	42.2	3234	6	BD205377 G protein
13	1745.2	42.2	3234	6	AX542191 Sequence
14	1745.2	42.2	3234	6	CQ714283 Sequence
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ALIGNMENTS

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DEFINITION Sequence 1 from patent US 6337391.  
ACCESSION AR182343  
VERSION AR182343.1 GI:20225259  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 4134)  
AUTHORS Harris,H.William., Brown,E.M. and Hebert,S.C.  
TITLE Polyclonal-sensing receptor in aquatic species and methods of use  
JOURNAL Patent: US 6337391-A 1 08-JAN-2002;  
FEATURES Location/Qualifiers  
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	Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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## RESULT 2

AR236221 LOCUS AR236221 Sequence 17 from patent US 6463883.

4134 bp DNA linear PAT 20-DEC-2002

ACCESSION AR236221

VERSION AR236221.1 GI:27280030

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 4134)

AUTHORS Harris,H.W. Jr., Russell,D.R., Nearing,J. and Betka,M.

TITLE Methods for raising pre-adult anadromous fish

JOURNAL Patent: US 6463883-A 17 15-OCT-2002;

FEATURES Location/Qualifiers

source 1..4134

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/mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 4134; DB 6; Length 4134;  
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source		i. .4134		/organism="unknown"		/mol_type="genomic DNA"	
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QY	241	GTTCACCTTTCTTGAGGATACGATCAACCTGGAAGGATGGAAGATTTGAGAGAA	300				
DB	241	GTTCACCTTTCTTGAGGATACGATCAACCTGGAAGGATGGAAGATTTGAGAGAA	300				
QY	301	ATGGGATTTGATCTTCCAGGATTTCTGTGTAAGGATCCCTACCAATTAAGATTA	360				
DB	301	ATGGGATTTGATCTTCCAGGATTTCTGTGTAAGGATCCCTACCAATTAAGATTA	360				
QY	361	GCAGAAATCTCCAGGATCTCTGTAACGGGCTGGGTAGTGGTCTCAAGAA	420				
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DB	1381	TTCCAGTGTGTCGGCGCACCATCGGCTTCTCAGGCGGGGGGTATCCACAGGTTTC	1440
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SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 4134)
AUTHORS	Harris,H.W. Jr., Russell,D.R., Nearing,J. and Betka,M.
TITLE	Methods for raising pre-adult anadromous fish
JOURNAL	Patent: US 6564747-A 17 20-MAY-2003;
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Db	2101	GTGCGG	CAACAG	GAAGGATCAT	CGAGGG	GAGCCAC	CTGCTG	CTTGAAT	GCATG	2160
QY	2161	GCATGT	GCAGAG	GAGAGTT	CAGTGT	GATGAAA	CGATG	CAAGTGC	GATCAAAAGTGCCG	2220
Db	2161	GCATGT	GCAGAG	GAGAGTT	CAGTGT	GATGAAA	CGATG	CAAGTGC	GATCAAAAGTGCCG	2220
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Db	2221	AATGAT	TTCTGGT	CGAATG	AGAACCA	CAGCTCGT	GCAATCG	CAAGGAG	ATCGAGTACCTG	2280
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QY	2461	ATCTTC	ATCGCG	AGCCAG	GGATCG	ACCTGT	CGCTCCG	CAACGG	CGCTTTGGCATC	2520
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QY	2641	CTGCTCT	CTCTG	CACTG	GTGCA	AAATCGT	CACTG	CAATCT	GTGCTCA	2700
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QY	2941	AGCA	ACCTAC	GGCA	AGTTTGT	GTGCG	CGGTG	AGTGA	TTCC	3000
Db	2941	AGCA	ACCTAC	GGCA	AGTTTGT	GTGCG	CGGTG	AGTGA	TTCC	3000
QY	3001	GGGCTG	CTGG	GCCTG	CACTT	ACTTCA	CAAGTGGT	TACAT	CACTG	3060

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QY	1861	CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACATTTGACGATCAAGGTGACCTCAAG	1920
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QY	1921	GGGAATACACCATATTAACATGGCAGCTCTCCGAGAGGATGAATCGTGTGTTCCAT	1980
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Db	2101	GTGCGGGGACCAAGAAAGGGATCATGAGGGGGAGCCCACTGCTGTTTGAATGCATG	2160
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QY	2221	AATGATTTCTGTCGAAATGAGAACCAACACGTGTCATCGCCAAAGGAGATCGAGTACCTG	2280
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QY	2641	CTGGTCTTCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATCTCTGTCATCTCTG	2700
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QY	2701	CCTCCCTCAGCTACAGGAACCATGAGCTGGAGGACGAGGTCATCTTCACTGAGTTCCTC	2760
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QY	2761	GAGGCTCGCTCATGCGGCTGGGCTTCTCATCGGCTACACCTGCTCTCTGCGGCAATC	2820
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QY	3601	TGCGGCTTCAAGCTTGGATCTTCTTCACTGCTGGATCTTCTTCACTCCCGCTATGTC	3660
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QY	3661	TCCTTCTTCAAGCTTGGATCTTCTTCACTGCTGGATCTTCTTCACTCCCGCTATGTC	3720
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QY	3721	ATAAGCTTCAAGCTTGGATCTTCTTCACTGCTGGATCTTCTTCACTCCCGCTATGTC	3780
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ORGANISM      Unknown.
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AUTHORS      Harris,H.W. Jr., Russell,D.R., Nearing,J. and Betka,M.
TITLE      Methods for raising pre-adult anadromous fish
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DEFINITION Sequence 17 from Patent WO0230182.
ACCESSION AX417770
VERSION AX417770.1 GI:215222908
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Haxris Jr, W. H., Betka, M., Russel, D. R. and Nearing, J.
TITLE Methods for raising pre-adult anadromous fish
JOURNAL Patent: WO 0230182-A 17 18-APR-2002;
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DEFINITION Sequence 23 from Patent WO0230215.
ACCESSION AX449101
VERSION AX449101.1 GI:21697918
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ORGANISM Mustelus canis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
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Triakidae; Mustelus.
REFERENCE 1
AUTHORS Harris,H.W., Russell,D.R., Nearing,J. and Betka,M.
TITLE Growing marine fish in freshwater
JOURNAL Patent: WO 0230215-A 23 18-APR-2002;
Aquadio Products Sciences, L.L.C. (US)
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ACCESSION AX743965
VERSION AX743965.1 GI:30722659
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SOURCE Squalus acanthias
ORGANISM Squalus acanthias
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squala; Hypnosqualea; Squaliformes; Squaloidei;
Squalidae; Squalus.
REFERENCE 1
AUTHORS Harris,J.H., Jury,S., Russel,D.R., Nearing,J., Betka,M., Linley,T.
and Brown,E.M.
TITLE Methods for growing and imprinting fish using an odorant
JOURNAL Patent: WO 03030639-A 7 17-APR-2003;
MARICAL, Inc. (US)
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QY 1441 AACAAAGTTCCTGAAGAGGTCCACCCAGCAGTCTCTCGGCAATGGGTTTGTCAAGGAG 1500  
DB 1441 AACAAAGTTCCTGAAGAGGTCCACCCAGCAGTCTCTCGGCAATGGGTTTGTCAAGGAG 1500  
QY 1501 TTCTGGAGGAGACCTTCAATGTCTATTACCGAGAGACCTTCAACAGCTGAAGAAT 1560  
DB 1501 TTCTGGAGGAGACCTTCAATGTCTATTACCGAGAGACCTTCAACAGCTGAAGAAT 1560  
QY 1561 TCCAAAGTGGCTTCGACGAGCCGCGCTCAAGGGGCGGCTCCAAAGCGGGGAGCTCC 1620  
DB 1561 TCCAAAGTGGCTTCGACGAGCCGCGCTCAAGGGGCGGCTCCAAAGCGGGGAGCTCC 1620  
QY 1621 AGACGAGCAGCCCTACGCCACCCCTGCACTGGGGAGAGAAATCACCAGAGGTGGAGACC 1680  
DB 1621 AGACGAGCAGCCCTACGCCACCCCTGCACTGGGGAGAGAAATCACCAGAGGTGGAGACC 1680  
QY 1681 CCCTACCTGGATATACACCTGAGGATCTCTCAATGATATAGTGGCGGTCTACTTCC 1740  
DB 1681 CCCTACCTGGATATACACCTGAGGATCTCTCAATGATATAGTGGCGGTCTACTTCC 1740  
QY 1741 ATTGTCTACGCCCTCGAAGACATCCACTCTTGCACAAACCCGCGAGGCTCTTTGCAAAAC 1800  
DB 1741 ATTGTCTACGCCCTCGAAGACATCCACTCTTGCACAAACCCGCGAGGCTCTTTGCAAAAC 1800  
QY 1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTTGGCAGGTCTCTCAACCAATCTGTGCAAT 1860  
DB 1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTTGGCAGGTCTCTCAACCAATCTGTGCAAT 1860  
QY 1861 CTGAAAGTTTACCAACAGCATGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920  
DB 1861 CTGAAAGTTTACCAACAGCATGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920  
QY 1921 GGGAACTACACCAATTAACCTGGAGCTCTCCGAGAGGATGAATCGGTGTGTTCAT 1980  
DB 1921 GGGAACTACACCAATTAACCTGGAGCTCTCCGAGAGGATGAATCGGTGTGTTCAT 1980  
QY 1981 GAGTGGGGCACTACAAAGCTTACGCTAAGCCAGTGAACCACTCAACCAATCAACGAAAG 2040  
DB 1981 GAGTGGGGCACTACAAAGCTTACGCTAAGCCAGTGAACCACTCAACCAATCAACGAAAG 2040  
QY 2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCAACTGAGTCAAGTGT 2100  
DB 2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCAACTGAGTCAAGTGT 2100  
QY 2101 GTGCCGGGACCAAGAAAGGATCATTCAGGGGGAGCCCACTGTCTTTGAATGCATG 2160  
DB 2101 GTGCCGGGACCAAGAAAGGATCATTCAGGGGGAGCCCACTGTCTTTGAATGCATG 2160

QY 2161 GCATGTGCAGAGGAGAGTTCAAGTATGATAAAGACATGCAAGATGGTGTGTAACAATGGCCG 2220  
DB 2161 GCATGTGCAGAGGAGAGTTCAAGTATGATAAAGACATGCAAGATGGTGTGTAACAATGGCCG 2220  
QY 2221 AATGATTTCTGGTGAATGAGAACCAACACCTCGTGCATCGCCAAAGAGATCGAGTACTG 2280  
DB 2221 AATGATTTCTGGTGAATGAGAACCAACACCTCGTGCATCGCCAAAGAGATCGAGTACTG 2280  
QY 2281 TCGTGAAGAGGAGGCTTCGGGATCGGTCTGACCAATCTTCGCCCTACTGGGCATCTGATC 2340  
DB 2281 TCGTGAAGAGGAGGCTTCGGGATCGGTCTGACCAATCTTCGCCCTACTGGGCATCTGATC 2340  
QY 2341 ACCTCTCTCTGCTGGGGGCTTCATCAAGTTTCAGGAACACTCCCATCTGTAAGGCCACC 2400  
DB 2341 ACCTCTCTCTGCTGGGGGCTTCATCAAGTTTCAGGAACACTCCCATCTGTAAGGCCACC 2400  
QY 2401 AACCGGAGTTGTCTACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCAGCTGCTC 2460  
DB 2401 AACCGGAGTTGTCTACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCTCAGCTGCTC 2460  
QY 2461 ATCTTCATCGCGAGCCAGGAGCTGGACCTGTTCGGCTCGGCCAACCGGCTTTGGCATC 2520  
DB 2461 ATCTTCATCGCGAGCCAGGAGCTGGACCTGTTCGGCTCGGCCAACCGGCTTTGGCATC 2520  
QY 2521 AGCTTCGTCTGTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580  
DB 2521 AGCTTCGTCTGTGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580  
QY 2581 GAGGCCAAGTTCGCCACAGCTTCCAGCCGCAAGTGGGTGGGCTTCAACCTGCGAGTTCTC 2640  
DB 2581 GAGGCCAAGTTCGCCACAGCTTCCAGCCGCAAGTGGGTGGGCTTCAACCTGCGAGTTCTC 2640  
QY 2641 CTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
DB 2641 CTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2700  
QY 2701 CCTCCCTCAGCTACAGGAACCATGAGTGGAGGAGAGGTCACTTTCATCAGCTGCGAC 2760  
DB 2701 CCTCCCTCAGCTACAGGAACCATGAGTGGAGGAGAGGTCACTTTCATCAGCTGCGAC 2760  
QY 2761 GAGGGCTCGCTACAGGCTGGGCTTCTCATCGGCTACAGCTTCTCGGGGCGCATC 2820  
DB 2761 GAGGGCTCGCTACAGGCTGGGCTTCTCATCGGCTACAGCTTCTCGGGGCGCATC 2820  
QY 2821 TGCTTCTTCTTCCGCTTCAAGTCCCGTAAAGTCCCGGAGAACTTCAACAGAGGTAAAGTTC 2880  
DB 2821 TGCTTCTTCTTCCGCTTCAAGTCCCGTAAAGTCCCGGAGAACTTCAACAGAGGTAAAGTTC 2880  
QY 2881 ATCACTTTCAGCATGTTGATCTTCTCATCGTCTGATCTCTTTCATCTCCCGCTATGTC 2940  
DB 2881 ATCACTTTCAGCATGTTGATCTTCTCATCGTCTGATCTCTTTCATCTCCCGCTATGTC 2940  
QY 2941 AGCACCTACGGCAAGTTTGTGCGCGGTGGAGGTGATTCGCAATCTTGGCTCCAGCTTC 3000  
DB 2941 AGCACCTACGGCAAGTTTGTGCGCGGTGGAGGTGATTCGCAATCTTGGCTCCAGCTTC 3000  
QY 3001 GGGCTGTGGGCTGCAATTTACTTCAACAAAGTGTATACATCATCTGTTCAAGCGCTGCCGT 3060  
DB 3001 GGGCTGTGGGCTGCAATTTACTTCAACAAAGTGTATACATCATCTGTTCAAGCGCTGCCGT 3060  
QY 3061 AACACATTCAGAGAGTGGCTGCGAGCGCGGCCCGCTTCAAGTGGGCGGCGG 3120  
DB 3061 AACACATTCAGAGAGTGGCTGCGAGCGCGGCCCGCTTCAAGTGGGCGGCGG 3120  
QY 3121 GCCACCTTCGGGCGCAGCGCGGTCTCGCAAGCGCTTCCAGAGCTTCTGCGGCTCCACC 3180  
DB 3121 GCCACCTTCGGGCGCAGCGCGGTCTCGCAAGCGCTTCCAGAGCTTCTGCGGCTCCACC 3180  
QY 3181 ATCTCTCGCCCGCTGCTCCACTGCGGGCGGGGCTTCAACATGAGATGAGAGCGGTGC 3240  
DB 3181 ATCTCTCGCCCGCTGCTCCACTGCGGGCGGGGCTTCAACATGAGATGAGAGCGGTGC 3240  
QY 3241 AGCAGCAGAGGTTCAGCTTTCGGCAGCGGCGCACCGTCAACCTGTCTGCTCAGCTTCGAGGAG 3300



QY 361 GCAGAAATCCTCCAGGCATCCTCTGTATAACCGGCTGGCGTAGTGTGGTTTGGTCAAGGAA 420  
Db 361 GCAGAAATCCTCCAGGCATCCTCTGTATAACCGGCTGGCGTAGTGTGGTTTGGTCAAGGAA 420  
QY 421 CAGAGACAGGGCTGCACAAATGCTCAGCTTCACTGCCAACTCTTATTCTTGGGATTTACA 480  
Db 421 CAGAGACAGGGCTGCACAAATGCTCAGCTTCACTGCCAACTCTTATTCTTGGGATTTACA 480  
QY 481 CTCCTACAGTCGTACAAATGCTCAGGGTATGGTCCAAACCAAGGGCCCAAGAAAGGA 540  
Db 481 CTCCTACAGTCGTACAAATGCTCAGGGTATGGTCCAAACCAAGGGCCCAAGAAAGGA 540  
QY 541 GACATCATCTGGGAGGCTCTTCCCAATACATTTGGAGTAGCGCCCAAGGATCAGGAC 600  
Db 541 GACATCATCTGGGAGGCTCTTCCCAATACATTTGGAGTAGCGCCCAAGGATCAGGAC 600  
QY 601 TTAAATCGAGACCGGAGCGCAAAATGATTTGGGTACAAATTTTCGAGGCTTCGGATGG 660  
Db 601 TTAAATCGAGACCGGAGCGCAAAATGATTTGGGTACAAATTTTCGAGGCTTCGGATGG 660  
QY 661 CTCGAGCGGATGATTTGCAATTTGAAGAGATTAAACAAGTATGACTTTCTGCCCAAT 720  
Db 661 CTCGAGCGGATGATTTGCAATTTGAAGAGATTAAACAAGTATGACTTTCTGCCCAAT 720  
QY 721 ATCACCTGGGATATCGCATATTTGACAGCTGTAAACCGTGTCCAAAGCGCTAGAGGCA 780  
Db 721 ATCACCTGGGATATCGCATATTTGACAGCTGTAAACCGTGTCCAAAGCGCTAGAGGCA 780  
QY 781 ACACCTCAGCTTTGTGGCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840  
Db 781 ACACCTCAGCTTTGTGGCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840  
QY 841 TGCTCTGACCATATCCCAATAGAGTACAGAGGCTTCCTGAGGACCATCCCAATGAT 1020  
Db 841 TGCTCTGACCATATCCCAATAGAGTACAGAGGCTTCCTGAGGACCATCCCAATGAT 1020  
QY 901 ACCGCTGTGGCCAACTTATTTGGGATTTATTTACATTTCCACAGGTCAGCTATGCTCTCCG 960  
Db 901 ACCGCTGTGGCCAACTTATTTGGGATTTATTTACATTTCCACAGGTCAGCTATGCTCTCCG 960  
QY 961 AGCAGGCTGCTCAGCAACAGAAATGAGTACAGGCTTCCTGAGGACCATCCCAATGAT 1080  
Db 961 AGCAGGCTGCTCAGCAACAGAAATGAGTACAGGCTTCCTGAGGACCATCCCAATGAT 1080  
QY 1021 GAGCAACAGGCCACGCGCATATGCGCAGATCATCGAGCATCTTCCAGTGAACCTGGGTGGGA 1080  
Db 1021 GAGCAACAGGCCACGCGCATATGCGCAGATCATCGAGCATCTTCCAGTGAACCTGGGTGGGA 1080  
QY 1081 ACCCTGGCAGCGCAGTACTATGCGCCGAGCATTTGACAAAGTTCCGGGAGGAGGCC 1140  
Db 1081 ACCCTGGCAGCGCAGTACTATGCGCCGAGCATTTGACAAAGTTCCGGGAGGAGGCC 1140  
QY 1141 GTTAGAGGGACATCTGTATTGACTTTCAGTGAGATGATCTCTCAGTACTACACCCAGAG 1200  
Db 1141 GTTAGAGGGACATCTGTATTGACTTTCAGTGAGATGATCTCTCAGTACTACACCCAGAG 1200  
QY 1201 CAGTTTGGAGTTTCAATCGCGGAGCTCATCCAGAACTCCTCGGCAAGGTCATCGTGTCTTC 1260  
Db 1201 CAGTTTGGAGTTTCAATCGCGGAGCTCATCCAGAACTCCTCGGCAAGGTCATCGTGTCTTC 1260  
QY 1261 TCCAAATGGCCCGGACCTGAGGCGGCTCATCAGGAGATAGTTTCGAGAAAATCACCGAT 1320  
Db 1261 TCCAAATGGCCCGGACCTGAGGCGGCTCATCAGGAGATAGTTTCGAGAAAATCACCGAT 1320  
QY 1321 CGGATCTGGCTGGCCAGGAGGCTTTGGGCGAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380  
Db 1321 CGGATCTGGCTGGCCAGGAGGCTTTGGGCGAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380  
QY 1381 TTCCACGTGGTGGCGGACCAATCGGCTTCAGGGCGGGCGGATCCCAAGGGTTC 1440  
Db 1381 TTCCACGTGGTGGCGGACCAATCGGCTTCAGGGCGGGCGGATCCCAAGGGTTC 1440

QY 1441 AACAAAGTTCTGAAGAGGTCCACCCAGCAGGTCTCCGGAACAATGGTTTGTCAAGGAG 1500  
Db 1441 AACAAAGTTCTGAAGAGGTCCACCCAGCAGGTCTCCGGAACAATGGTTTGTCAAGGAG 1500  
QY 1501 TTCTGGGAGGAGACCTTTCAACTGCTACTTCAACGAGAAAGACCTGACGAGCTGAAGAAT 1560  
Db 1501 TTCTGGGAGGAGACCTTTCAACTGCTACTTCAACGAGAAAGACCTGACGAGCTGAAGAAT 1560  
QY 1561 TCCAAAGTGCCTTCGACACGGAACCGGGGCTCAAGGGGACGGCTCCAAAGCGGGGAACTCC 1620  
Db 1561 TCCAAAGTGCCTTCGACACGGAACCGGGGCTCAAGGGGACGGCTCCAAAGCGGGGAACTCC 1620  
QY 1621 AGAGGACACGCTAGCCACCCCTGCACCTGGGAGGAGAAACATCACAGCGTGGAGACC 1680  
Db 1621 AGAGGACACGCTAGCCACCCCTGCACCTGGGAGGAGAAACATCACAGCGTGGAGACC 1680  
QY 1681 CCCTACCTGGATTTATACACACCTGAGGATCTCTCTACAATGTATACGTGGCGCTACTCC 1740  
Db 1681 CCCTACCTGGATTTATACACACCTGAGGATCTCTCTACAATGTATACGTGGCGCTACTCC 1740  
QY 1741 ATTGCTCAGCCCTGCAGACATCCACTTTTGCAAAACCGGGCACGGGCATCTTTGCAAAAC 1800  
Db 1741 ATTGCTCAGCCCTGCAGACATCCACTTTTGCAAAACCGGGCACGGGCATCTTTGCAAAAC 1800  
QY 1801 GGATCTTGTGCAGATTTAAAAAGTTGAGGCTTGCAGGTCTCTCAACCATCTGCTGCAT 1860  
Db 1801 GGATCTTGTGCAGATTTAAAAAGTTGAGGCTTGCAGGTCTCTCAACCATCTGCTGCAT 1860  
QY 1861 CTGAAGTTTACCAACAGCATGGGTGAGAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920  
Db 1861 CTGAAGTTTACCAACAGCATGGGTGAGAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920  
QY 1921 GGGAACTTACACCATTTCAACTGCGAGCTCTCCGAGAGGATGAATCGGTGTTGTCCAT 1980  
Db 1921 GGGAACTTACACCATTTCAACTGCGAGCTCTCCGAGAGGATGAATCGGTGTTGTCCAT 1980  
QY 1981 GAGTGGGCAACTCAACCGCTACGCTAAGCCAGTACCGACTCAACATCAACGAAAG 2040  
Db 1981 GAGTGGGCAACTCAACCGCTACGCTAAGCCAGTACCGACTCAACATCAACGAAAG 2040  
QY 2041 AAAATCTCTGGAGTGGCTTCTCCAAAGTGGTTCTTCCAACTGCACTGCTGATGATG 2100  
Db 2041 AAAATCTCTGGAGTGGCTTCTCCAAAGTGGTTCTTCCAACTGCACTGCTGATGATG 2100  
QY 2101 GTGCGGGCACAGGAGGAGATCATCGAGGGGAGGCCACCTGCTTGAATGCATG 2160  
Db 2101 GTGCGGGCACAGGAGGAGATCATCGAGGGGAGGCCACCTGCTTGAATGCATG 2160  
QY 2161 GCATGTGCAGAGGAGGATTCAGTGAATAAAGATGCAAGTGCCTGTACAAAGTGCCCG 2220  
Db 2161 GCATGTGCAGAGGAGGATTCAGTGAATAAAGATGCAAGTGCCTGTGTACAAAGTGCCCG 2220  
QY 2221 AATGATTTCTGGTTCGATGAGAACACAGTGCCTGATCGCCAAAGGAGATCGAGTACCTG 2280  
Db 2221 AATGATTTCTGGTTCGATGAGAACACAGTGCCTGATCGCCAAAGGAGATCGAGTACCTG 2280  
QY 2281 TCGTGGACGAGCCCTTCGGGATCGCTCTGACCATCTTCCCGTACTGGGCATCTGATC 2340  
Db 2281 TCGTGGACGAGCCCTTCGGGATCGCTCTGACCATCTTCCCGTACTGGGCATCTGATC 2340  
QY 2341 ACCTCTCTGCTGGGGTCTTTCATCAAGTTTCAGAACTCTCCATCTGCTGCTTCTCCAGCTCGCTC 2400  
Db 2341 ACCTCTCTGCTGGGGTCTTTCATCAAGTTTCAGAACTCTCCATCTGCTGCTTCTCCAGCTCGCTC 2400  
QY 2401 AACCGGAGTTGCTCTACCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460  
Db 2401 AACCGGAGTTGCTCTACCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460  
QY 2461 ATCTTCAATCGGCGAGCCAGGAGTCTGAGCTGTCCGCTCGCCCAACCGGCTTTGGCATC 2520  
Db 2461 ATCTTCAATCGGCGAGCCAGGAGTCTGAGCTGTCCGCTCGCCCAACCGGCTTTGGCATC 2520  
QY 2521 AGCTTCGCTGCTGATCTCTCTGATCTCTGATGAGAACCAACCGGCTGCTGCTGCTTCTC 2580



Query Match		42.2%;	Score 1745.2;	DB 6;	Length 3234;
Best Local Similarity		76.4%;	Pred. No. 7.6e-273;		
Matches 2187;		Conservative	0;	Mismatches 658;	Indels 17; Gaps 3;
Qy	501	CTCAGGATGTGTCACAAACCAAGAGGCGCCAGAGGAGAGACATCATACATCTGGAGGTCT	560		
Db	51	CTCTGCTACGGCCAGACACAGCAGCCCAAGAGAGGAGGACATATCTCTGGGGGCT	110		
Qy	561	CTTCCCAATACACTTGGAGTAGCCCGCAAGGATCAGGACTTAAATCGAGACCGAGGC	620		
Db	111	CTTTCTTATTCATTTTGGAGTAGCAGCTAAAGATCAAGATCTCAATCAAGGCCGGAGTC	170		
Qy	621	GACAAATGTATTCGGTCAATTTTCGAGGCTTCGATGGTCCAGGCGATGATATTCGC	680		
Db	171	TGTGAAATGTATCAGGTATATTTCCGTGGGTTTCGCTGGTACAGGCTATGATATTCG	230		
Qy	681	AATTGAAGAGATTAACAACAGATGACTTTCTGCCCCAATATCAACCTGGGATATCGCAT	740		
Db	231	CATAGAGAGATTAACAACAGCAGCCAGCCCTCTTCCCAACTTGACGCTGGGATACAGGAT	290		
Qy	741	ATTTGACAGCTGTACACCGTGTCCAGGCGTAGAGGCAACACTCAGCTTTGTGGCCCA	800		
Db	291	ATTTGACACTTGCACACCGTTTCTAAGCCCTTGAAGCCACCCCTGAGTTTGTGTCTCA	350		
Qy	801	GAAACAAATTCGACTCGCTGAACCTTAGATGAGTTCTGTAACTGCTCTGACCATATCCCATC	860		
Db	351	AAACAAATTTGATCTTTGAACTTGTATGAGTTCTGCAACTGCTCAGAGCACATTCCTC	410		
Qy	861	CACATAGAGTGTGCGGGCNAACCGGTTCAGGAATCTCCAGGCTGTGGCCATCTATT	920		
Db	411	TACGATCTCTGTGGGAGCAACTGGCTCAGGCGTCTCCAGCGAGTGGCAAAATCTGCT	470		
Qy	921	GGGATTTATTTACATTCACAGGTGAGTATGCTCTCCCTCGAGCAGGCTGCTCAGCAACA	980		
Db	471	GGGGCTCTTACATTTCCCAAGTCAGTTATGCTCTCTCCAGCAGACTCTCTCAGCAACA	530		
Qy	981	GAAAGAGTAAAGGCTTCTGAGGACCATCCCCAATGATGAGCAACAGGCCACGGCAT	1040		
Db	531	GAAACAATTCAGTCTTCTCCGAAACCATCCCCAATGATGAGCAACAGGCCACTGGCAT	590		
Qy	1041	GGCCAGATCATCAGACTTCCAGTGAACTGGTGGGAACTTGGGAGGAGCCCTGGCAGCCGACGATG	1100		
Db	591	GGCAGACATCATGAGTATTTCCGCTGGAACTGGGTGGGCAATTTGAGCTGATGAGCA	650		
Qy	1101	CTATGGCCGCCAGGCAATGACAACTTCCGGAGGAGGCGCTTAAAGAGGACATCTGTAT	1160		
Db	651	CTATGGCGCGCGGGATTTGAGAAATTCGAGAGGAGAACTGAGGAAAGGGATATCTGCAT	710		
Qy	1161	TGACTTCAGTGAATGATCTCAGTACTACCCAGAGGAGTGGAGTTTCACTGCGCA	1220		
Db	711	CGACTTCAGTGAATCATCTCCAGTACTCTGATGAGGAGAGATCCAGCATGTGGTAGA	770		
Qy	1221	CGTCAATCAGAACTCTCGGCCAAGTCAATCGTGTCTTCTCCAAATGGCCCGACCTGGA	1280		
Db	771	GGTGATTCAAATTCACGGCCAAAGTCAATCGTGGTTTCTCCAGTGGCCAGATCTTGA	830		
Qy	1281	GCCGCTCATCCAGGAGATGTTCGAGAAACATCACCGATCGGATCTGGCTGGCCAGCA	1340		
Db	831	GCCCCATCATCAAGGAGATGTTCGCGGCAATATCACGGGCAAGATCTGGCTGGCCAGCA	890		
Qy	1341	GGCTTGGCCAGCTCTCGCTCATTTGCCAGCCAGGACTTCCACGTGGTCTGGGGCAC	1400		
Db	891	GGCCTGGCCAGCTCTCTCGATCGCCATGCTCCTCAGTACTTCCACGTGGTGGGGCAC	950		
Qy	1401	CATCGGCTTCTCAGGGGGGCGTATCCCCAGGGTTCAACAGTTTCTTGAAGGAGGT	1460		
Db	951	CATTGGATTCGCTCTGAAGGCTGGCCAGATCCCCAGGCTTCCGGAAATTCCTGAAGAGGT	1010		
Qy	1461	CCACCCAGCAGGTCTCGGCAATGGGTTTGTCAAGAGTTCTGGAGGAGACCTTCAA	1520		
Db	1011	CCATCCAGGAGTCTGTCCAAATGGTTTTCGCAAGGAGTTTGGGAAAGAACATTTAA	1070		

Qy	1521	CTGCTACTTCCACCGAGAGACCTGAGCGAGCTGAAGAAATTCCAAGGTGCTCGACGG	1580		
Db	1071	CTGCCACTTCAAAGA-----AGGTGCAAAAGGACCTTTTACTGTGGACACCTTTCTG	1122		
Qy	1581	ACCGCGGCTCAAGGGGACGGCTCCAAAGCGGGGAACTCCAGACGGACGCCCTACGCCA	1640		
Db	1123	AGAG-----TCAAGAAAGTGGCGACAGTTTAGCAACAGCTCGACAGCTTCGGACC	1178		
Qy	1641	CCCTGCACTGGGAGGAGNACATCACCAGCTGGAGACCCCTACTCGATTATACACA	1700		
Db	1179	CTCTGTACAGGGGATGAGAAACATCAGCAGTGTGAGAGACCCCTTACATAGATTACAGCA	1238		
Qy	1701	CTGAGGATCTCTACAATGTAACGTGGCGCTACTCTCAATGCTCAGGCCCTGCAAGA	1760		
Db	1239	TTTACGGATATCTCAATGTGTACTTAGCAGTCTACTCCATTTGCCACGCCCTTGAAGA	1298		
Qy	1761	CATCCACTTTTGAACACCCGGACGGGCACTTTTGGAAACGGATCTGTGTGAGATATTA	1820		
Db	1299	TATATATACCTGTACTCTGGAGAGGGCTCTTACCAATGGCTCTGTGTGAGACATCAA	1358		
Qy	1821	AAAAGTTGAGCGCTGCGCAGGTCTCAACATCTGTCATCTCAAGTTTACCAACAGCAT	1880		
Db	1359	GAAAGTTGAGCGTGGCAGGTCTCTGAAGCACCTACGGCATCTTAACTTTACAAACAATAT	1418		
Qy	1881	GGGTGACAGTTGACTTTTGAAGTCAAGGTGACCTCAAGGGGAACTACACCAATTACAA	1940		
Db	1419	GGGGAGCAGTGCATCTTTGATGAGTGTGTGACCTGGTGGGAACTATTCCATCATCAA	1478		
Qy	1941	CTGGCAGCTCTCGCAGAGAGATGAATCGGTGTGTTTCCATGAGGTGGGCAACTACACGC	2000		
Db	1479	CTGGCAGCTCTCGCAGAGAGATGGCTCCATCTGTTTAAAGAAAGTGGGTATTACACGT	1538		
Qy	2001	CTAGCTTAAGCCAGTGACCGACTCAACATCAACGAAAGAAATAATCTCTGGAGTGGCTT	2060		
Db	1539	CTATGCCAAGAGGAGAAAGACTCTTTCATCAACGAGGAGAAATAATCTGTGGAGTGGTT	1598		
Qy	2061	CTCAAGAGTGGTCTTTCTTCCAACTGCGAGTCAAGCTGTGTGCCGGGCAACAGGAAGG	2120		
Db	1599	CTCAGGAGGTGCTCTTCTCAACTGCGAGCCGAGCTGCTGCGCAGGAGCCAGGAAGG	1658		
Qy	2121	GATCATGAGGGGAGCCACCTGCTGCTTTGAAATGCTGGCATGTGCGAGGGGAGATT	2180		
Db	1659	GATCATGAGGGGAGCCACCTGCTGCTTTGAGTGTGTGAGTGTCTGTATGGGAGTA	1718		
Qy	2181	CAGTGATGAAACGATGCAAGTGCCTGTATAAAGTCCCGAAATGATTTCTGTGCAATGA	2240		
Db	1719	TAGTGATGAGACAGATGCCAGTGCCTGTAAAGTCCCGAGATGACTTCTGTGCCAATGA	1778		
Qy	2241	GAACCAACGCTGCTGATCGCAAGAGATCGAGTACCTGTGTGAGCAGCGCCCTCGG	2300		
Db	1779	GAACCAACCTCTGCTGCTTGGCAAGGAGATCGAGTTTCTGTGAGCAGGAGCCCTTGG	1838		
Qy	2301	GATCGCTCTGACCATCTTGGCCGTACTGGGCGATCTCTGATCACCTCTTGTGTGGGGT	2360		
Db	1839	GATCGCACTCACCTCTTTGGCGTGTGGGCAATTTTCTTGACAGCCTTTGTGCTGGGTGT	1898		
Qy	2361	CTTCAATCAAGTTGAGAAACACTCCCATCGTGAAGGCGCACCAACCGGGAGTTGTCTACCT	2420		
Db	1899	GTTTATCAAGTTCCGAAACACACCCATTTGAAGGCGCACCAACCGAGAGCTCTCTACCT	1958		
Qy	2421	GCTGCTCTTCTCCCTCATCTGTGCTTCTCCAGTCCGCTCATCTTCACTCGGAGGCCAG	2480		
Db	1959	CTTCTCTTCTCTCTCTCTGCTCTTCTCCAGTCCCTGTCTTCTCATCGGAGGCCCA	2018		
Qy	2481	GGACTGAGCCTGTGCGCTCGGCAACCGGCTTTTGGCATCAGCTTCTGTGCAATCTC	2540		
Db	2019	GGACTGAGCCTGTGCGCTCGGCGAGCGGCTTTTGGCATCAGCTTCTGTGCTCTGCTC	2078		
Qy	2541	CTGCATCTCTGTAAGACCAACCGGCTGTGCTGCTTTCGAGGCCCAAGATCCCAACAG	2600		
Db	2079	ATGCATCTCTGTAAGACCAACCGCTGCTCTCTCTGCTTTCGAGGCCCAAGATCCCAACAG	2138		
Qy	2601	CTCCACCGCAAGTGGGTGGGCTCAACCTGCAGTTTCTCTCTGCTCTCTCTGCTCTCT	2660		



Db	2139	CTTCCACCGCAAGTGGTGGGGCTCAACTGAGTCTCTGGTTTCTCTGCACCTT	2198
Qy	2661	GGTGAAATCGTCACTGATCATCTGGCTTACACCGGGCTCCTCCAGCTACAGAA	2720
Db	2199	CATGAGATTGTATCTGTGTATCTGGCTTACACCGGGCTCCTCAAGCTACCGAA	2258
Qy	2721	CCATGAGCTGGAGGAGGATCATCTTCACTACCTCGACGAGGGCTCGCTCATGGCT	2780
Db	2259	CCAGAGCTGGAGGATGATCATCTTCACTGAGTCCACGAGGGCTCCTCATGGCT	2318
Qy	2781	GGGCTTCTCATCGGCTACACCTGCTCCTCGCGCCATCTGCTTCTTTCGCTTCAA	2840
Db	2319	GGGCTTCTCATCGGCTACACCTGCTCCTCGCGCCATCTGCTTCTTTCGCTTCAA	2378
Qy	2841	GTCCGTAAGCTGCGGAGAACTTCAACGAGCTAAGTTCATCAGCTTCAGCATGTTGAT	2900
Db	2379	GTCCGGAAGCTGCGGAGAACTTCAATGAGCCCAAGTTCATCAGCTTCAGCATGTTGAT	2438
Qy	2901	CTTCTTTCATCGTCTGATCTCTCTTCACTCCCGCTTATGTACAGCACTACGGCAAGTTGT	2960
Db	2439	CTTCTTTCATCGTCTGATCTCTCTTCACTCCAGCTTATGCCAGCACTATGGCAAGTTGT	2498
Qy	2961	GTCCGCTGGAGGATGATTGCCATCTGGCTTCCAGCTTCCGGCTGCTGGGCTGCAITTA	3020
Db	2499	CTCTGCCGTAGAGTGAATGCCATCTGGCAGCCAGCTTGGCTTGTGGGCTGCAITTT	2558
Qy	3021	CTTCAACAGTGTATCATCATCTCTTCAAGCGTGGCGTAAACACATCGAGGAGTGGC	3080
Db	2559	CTTCAACAGTGTATCATCATCTCTTCAAGCGTGGCGTAAACACATCGAGGAGTGGC	2618
Qy	3081	CTCAGCAGCGCGCCACGCTTCAAGTGGCGCGCGGCCACCTCTCGCGCGAGCGC	3140
Db	2619	TTGCAGCAGCGCTCAGCTTCAAGTGGCGCGCGGCCACCTCTCGCGCGAGCGC	2678
Qy	3141	CGGCTCTCGAGCGCTCAGCAGCTGTGGCTTCCACCATCTCTCGCGCGCTCGTC	3200
Db	2679	CGTCTCCGCAAGCGTCCAGCAGCTTGGAGGCTTCCAGGATCCACCCCTCTCTCTC	2738
Qy	3201	CACCTCGCGCGCGGCTCACCATCGAGATGAGCGCTGAGCAGCAGAGAGTTCAGCTT	3260
Db	2739	CATCAGCAGCAGAGCAACA-----GCGAAGACCCATCCACAGCCCGAGAGG	2793
Qy	3261	CGCAGCGGCAAGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3320
Db	2794	CAGCAGCAGCGCTGGCCCTTACCCAGCAAGAGCAGCAGCAGCAGCAGCAGCAGC	2853
Qy	3321	CAGCGCAGCGCGCGCAGCAGCACTCGCGGATGCGCGCAG	3362
Db	2854	CAGCAGCAAGTCTCAGCAGCAGCCAGATGCAAGCAGAG	2895

RESULT 13  
 AX542191  
 LOCUS  
 DEFINITION  
 Sequence 18 from Patent WO0229033.  
 AX542191  
 VERSION  
 AX542191.1 GI:25276404  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)  
 Homo sapiens  
 Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1  
 Stormann, T., Hammerland, L.G., Storjohann, L.L., Busby, J.G.,  
 Garrett, J.E. and Simin, R.T.  
 G-protein fusion receptors and chimeric gaba b? receptors  
 Patent: WO 0229033-A 18 11-APR-2002;  
 NPS PHARMACEUTICALS, INC. (US)  
 Location/Qualifiers  
 1..3234  
 /organism="Homo sapiens"  
 /mol\_type="unassigned DNA"

ORIGIN	/db_xref="taxon:9606"			
Query Match	42.2%;	Score 1745.2;	DB 6;	Length 3234;
Best Local Similarity	76.4%;	Pred. No. 7.6e-273;		
Matches 2187;	Conservative 0;	Mismatches 658;	Indels 17;	Gaps 3;
Qy	501	CTCAGGGTATGGTCCAAAACCAAGGGCCAGAGAAAGAGAGACATCATATCTGGAGGTCT	560	
Db	51	CTCTGCCTCAGGGCCAGACAGGAGGCCCAAGAGGGGGACATTATCTCTGGGGGCT	110	
Qy	561	CTTCCCAATACACTTTGGAGTAGCGGCCAAGGATCAGGACTTAAATTCGAGACCGGAGGC	620	
Db	111	CTTTCCTATTCAITTTGGAGTAGCAGCTAAAGATCAAGATCTCAATCAAGCGCGAGTC	170	
Qy	621	GACAAATGATTTCGGTACAAATTTTCAGAGCTTCCGATGGCTCCAGGCGATGATATTCGC	680	
Db	171	TGTGGAATGATCAGGTATTAATTTCCGTGGGTTTCGCTGGTTACAGGCTATGATATTTGC	230	
Qy	681	AATTGAGAGATTAAACAAACAGTATGACTTTCCTGCCCAATATCACCTCGCATATCGCAT	740	
Db	231	CATAGAGGAGATAAACAGAGCCAGCCCTTCTTCCCACTTGAAGCTGGGATACAGGAT	290	
Qy	741	ATTGACAGCTGTAACACCGTGTCCAGGCGCTAGAGGCAACACTCAGCTTTGTGGCCCA	800	
Db	291	ATTTGACACTTGCAACACCGTTTCTAAGGCTTTGGAAAGCCACCGCTGAGTTTGTGCTCA	350	
Qy	801	GAACAAATCGACTCGCTGAACCTTAGATGAGTTCTGTAACTCTGACCATATCCCATC	860	
Db	351	AAACAAATTTGATTTCTTGAACCTTGAAGTTTCTGCACTGCTCAGAGCAGATTCCTC	410	
Qy	861	CACAAATAGCAGTGGTTCGGGGCAACCGGGTCAGGAATCTCCAAGGCTGTGGCCAAATCTATT	920	
Db	411	TACGATTTGCTGGTGGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAAAATCTGCT	470	
Qy	921	GGGATTAATTTACATTTCCACAGGTGAGTATGCTCTCTCGAGCAGGCTGCTCAGCAACA	980	
Db	471	GGGGCTCTTCTACATTTCCCGAGTCACTTATGCTCTCTCCAGCAGACTCTCTCAGCAACA	530	
Qy	981	GAATGAGTCAAGGCTTCTCTGAGGACCATCCCAATGATGAGCAACAGAGCCACGGCCAT	1040	
Db	531	GAATCAATTCAGTCTTCTCTCGAACCATCCCAATGATGAGCAACAGAGCCACTGCCAT	590	
Qy	1041	GGCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGAAACCTTGGCAGCCGACGATGA	1100	
Db	591	GGCAGACATCATCGAGTATTTCCGCTGGAACTGGGTGGGCACAATTCGACCTGATGACGA	650	
Qy	1101	CTATGGCGGCCAGGCAATTGACAAAGTTCCGGGAGGAGGCGGTTAAGAGGACATCTGTAT	1160	
Db	651	CTATGGCGGCCGGGGATTGAGAAATTCGAGAGGAGCTGAGGAAAGGATATCTGCAT	710	
Qy	1161	TGACTTCAGTGAATGATCTCTCAGTACTACACCCAGAGCAGTTGGAGTTCAATTCGCCGA	1220	
Db	711	CGACTTCAGTGAATCATCTCCAGTACTCTGATGAGGAAAGATCCAGCATGTGTGATGA	770	
Qy	1221	CGTCACTCCAGAACTCTCGGCCAAGTTCATCTGGTCTTCTTCCAAATGGCCCGACCTGGA	1280	
Db	771	GGTGATTCAAATTCACGGCCAAAGTTCATCTGGTGGTTTCTCCAGTGGCCAGATCTTGA	830	
Qy	1281	GCCTGCTCATCCAGGAGATGTTTCGGAGAAACATCACCGATTCGATCTGGTGGCCAGCGA	1340	
Db	831	GCCTCATCAAGGAGATTTCCGGCGCAATATCACGGGCAAGATCTGGTGGCCAGCGA	890	
Qy	1341	GGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTACTTCCAGTGGTGGCGGCAC	1400	
Db	891	GGCTTGGCCAGCTCTCTCCGTGATTCGCTATCCCTCAGTACTTCCAGTGGTGGCGGCAC	950	
Qy	1401	CATCGGCTTCGCTCTCAGGCGGGGGCTATCCACAGGGTTCAACAAGTTCTCTGAAGAGGT	1460	
Db	951	CAITGGATTTCGCTCTGAAGGCTGGGAGATCCACGGCTTCCGGGAAATTCCTGAAGAGGT	1010	
Qy	1461	CCACCCAGCAGGTCCTTCGGAACAATGGGTTTGTCAAGAGTTCTTGGAGGAGACCTTCAA	1520	



Db 1011 CCATCCCAAGAGTCTGTCCAAATGGTTTGGCCAAAGAGTTTGGGAGAAACATTTAA 1070  
Qy 1521 CTGTACTTACCGAAGAGACCTCACGACAGCTGAAGAAATCCAAAGTGCCTCGCACGG 1580  
Db 1071 CTGCCACCTCCAGA-----AGTGCAAAAGGACCTTTACCTGTGACACCTTTCTG 1122  
Qy 1581 ACCGGGGCTCAAGGGGACGGCTCAAGCGGGGAACTCCAGACGAGACCCCTACGGCA 1640  
Db 1123 AGAGG----TCACGAAGAAGTGGCGGACAGGTTTAGCAACAGCTCGACAGCCCTCCGACC 1178  
Qy 1641 CCCCTGCACTGGGGAGGAGAACATCACAGCGCTGGAGACCCCTACCTGGATTTATACACA 1700  
Db 1179 CCTCTGTACAGGGGATGAAACATCAGCAGTGTGAGACCCCTTACATAGATTACAGCA 1238  
Qy 1701 CTTAGGATCTCCTCAATGTATAGTGGCCGTCTACTCCATGCTCAGCCCTGCAAGA 1760  
Db 1239 TTTACGGATATCTCAATGTGTACTTAGCAGTCTACTCCATTGCCACGCTTGGCAAGA 1298  
Qy 1761 CATCCACTTTGCAAAACCGGACAGGGCATCTTTGCCAAACGATCTTTGTCAGATTTAA 1820  
Db 1299 TATATATACCTCTTACCTTGGGAGAGGCTCTTACCAATGGCTCTGTGAGACATCAA 1358  
Qy 1821 AAAAGTTAGGCGCTGGCAGGTCTCTCAACCATCTGCTGATCTGAAAGTTTACCAACAGCAT 1880  
Db 1359 GAAAGTTAGGCGGTGGCAGGCTCTGAAGCACCTACGGCATCTAATCTTTACAAACAATAT 1418  
Qy 1881 GGTGAGCAGGTTGATTTTGACATCAAGTGACCTCAAGGGAACTACACATATACAA 1940  
Db 1419 GGGGAGCAGGTGACCTTTTGATGAGTGTGGTACCTGTGGGAACTATTCCATCATCAA 1478  
Qy 1941 CTGGCAGCTCTCCGACAGAGATGAATCGGTGTGTTTCCATGAGTGGGCACTACAAGC 2000  
Db 1479 CTGGCACCTCTCCACAGAGATGGCTCCATCGTGTTTAAGGNAAGTCGGGTATTACAACT 1538  
Qy 2001 CTACGCTAAGCCAGTGACCGACTCAACATCAACGAAAGAAATCTCTGTGAGTGGCTT 2060  
Db 1539 CTATGCAAGAGGAGAAAGACTCTTCAACACGAGGAGAAATCTCTGTGAGTGGCTT 1598  
Qy 2061 CTCGAAAGTGTCTCTCTCAACTGCAGTGCAGACTGTGCGGGCACACAGGAGGG 2120  
Db 1599 CTCGAGGAGGTGGCTCTCTCAACTGCAGCGGAGACTGCTGGCAGGAGCAGGAAAG 1658  
Qy 2121 GATCATCAGAGGGGAGCCACCTGTCTTGAATGCATGGCATGTGAGAGGGAGATT 2180  
Db 1659 GATCATGAGGGGAGCCACCTGTCTTGAATGTGTGGAGTGTCTGTATGGGAGTA 1718  
Qy 2181 CAGTGATGAAACGATGCAAGTGGCTGTACAAAGTGGCCGATGATTTCTGTGTCGAATGA 2240  
Db 1719 TAGTGATGAGACAGATGCCAGTGCCTGTAAACAGTGCCAGATGACTTCTGTGTCGAATGA 1778  
Qy 2241 GAACACACGTCGTGCATCGCAAGAGATCGAGTACCTGTGTCGAGCGAGCCCTTCGG 2300  
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Qy 2301 GATCGTCTGACCATTTCCCGTACTGGGCATCTGTGATCACTCTTGTGTGGGGT 2360  
Db 1839 GATCGCACTCACCTCTTTCGGCTGTGGGCATTTTCTGACAGCTTTGTGTGGGTGT 1898  
Qy 2361 CTTTCATCAAGTTCAGGAACATCCCATCGTGAAGCCACACCGGAGTGTCTTACTCT 2420  
Db 1899 GTTATCAAGTTCGGCAACACACCCATTTCAAGGCCACCAACCGAGAGCTCTCTACT 1958  
Qy 2421 GTGTCTCTTCTCCCTCATCTGTGTCTTCTCAGCTCGCTCATCTTCACTGGGAGCCGAG 2480  
Db 1959 CTTCTCTTCTCCCTGCTCTGTGCTTCTCCAGCTCCCTGTTCTTCACTGGGAGCCCA 2018  
Qy 2481 GAGTGGACCTGTGGCTCGGCAACCGGCTTTGGCATCAGCTTGTGCTGTGATCTC 2540  
Db 2019 GAGTGGACGTGGCTCGGCGAGCCGCTTTGGCATCAGCTTGTGCTGTGATCTC 2078  
Qy 2541 CTGCATCTCTGTAAGCAACCGGCTGTGTGTTCTTCGAGGCAAGATCCCCACAG 2600  
Db 2079 ATGCATCTCTGTAAGCAACCGGCTGTGTCTCTGTGTTTGAAGCCAGATCCCCACAG 2138

Qy 2601 CTTCCACCGAAGTGGGTGGGCTCAACCTGCAAGTTCTCTGGTCTTCTCTGATCTCT 2660  
Db 2139 CTTCCACCGAAGTGGGTGGGCTCAACCTGCAAGTTCTCTGGTCTTCTCTGATCTCT 2198  
Qy 2661 GGTGCAATCGTCACCTGCATCATCTGGCTCTACACGGCGCTCCCTCCAGCTACAGGAA 2720  
Db 2199 CATGCAATGTCTCATCTGTGATCTGGCTCTACACGGCGCTCCCTCAAGCTACGCAA 2258  
Qy 2721 CCATGAGCTGAGAGGAGGTCTTTCATCAGCTGCGAGGGGTCTGCTCATGCGCT 2780  
Db 2259 CCAGGAGCTGAGGATGAGATCATCTTTCATCAGCTGCGAGGGGTCTCCCTCATGGCCT 2318  
Qy 2781 GGGCTTCTCATCGGCTACACCTGCTCTCCGCGCATCTGCTTCTTCTGCTTCAA 2840  
Db 2319 GGGCTTCTCATCGGCTACACCTGCTCTCCGCGCATCTGCTTCTTCTGCTTCAA 2378  
Qy 2841 GTCCGCTAAGCTCGCGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTTGAT 2900  
Db 2379 GTCCGGAAGCTCGCGAGAACTTCAAGAGCAAGTTTCATCACCTTCAGCATGTCAT 2438  
Qy 2901 CTTCTTCATCGTGTGATCTCTTTCATCCCGCTATGTGAGACCTACGCGCAAGTTGT 2960  
Db 2439 CTTCTTCATCGTGTGATCTCTTTCATCCAGCTATGCGAGACCTATGCGCAAGTTGT 2498  
Qy 2961 GTCCGCGTGGAGTGTATTCGCTCTGCTTCCAGCTTCCGGCTGCTGGGCTGCATTTA 3020  
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Qy 3021 CTTCAACAAGTGTATCATCTCTTTCAGCGCTGCGCTAACCACTCAGAGGTGCG 3080  
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Qy 3081 CTGACAGCAGCGGCGCCACCTTCAAGTGGCGCGCGGCGCACCTCCGCGCGAGCAA 3140  
Db 2619 TTGACAGCAGCGCTCACCTTTCAGGTGGCTGCGCGCGCGCACCTGCGCGCGAGAA 2678  
Qy 3141 CGCTCTCGCAAGCGCTCCAGCAGCTGTGCGGCTCACCATCTCTCTGCGCGCTCGTC 3200  
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Qy 3201 CACTGCGCGCGGCTCTACCATGAGATGCAAGCTGAGCGCTGACGACGAGAGGTGAGCTT 3260  
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Qy 3261 CGGACAGCGCACCTGCTACCTGCTGCTCAGCTTTCGAGGACAGGCGGATACGCCACCT 3320  
Db 2794 CAGCAGCAGCGCTGCGGCTTAACTCCAGCAAGAGCAGCAGGAGCCCTGACCTCCA 2853  
Qy 3321 CAGCGCACGCGCGCAGCAGGAACTCGCGGATGCGCGAG 3362  
Db 2854 CAGCAGCAAGTCTCAGCAGCAGCCAGATGCAAGCAGAAG 2895

RESULT 14  
CO714283  
LOCUS 3783 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 217 from Patent WO02068579.  
ACCESSION CO714283  
VERSION CO714283.1 GI:42275140  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
Venter, C.J., Adams M.C., Li, P.W. and Myers, E.W.  
Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
Patent: WO 02068579-A 217 06-SEP-2002; /  
PE Corporation (NY) (US)  
JOURNAL Location/Qualifiers  
FEATURES

source	1. .3783																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
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2541	QY	CTG	CAT	CTCTGGTGAAGACAA	CCGGT	GCTGCTGGTCTTCGAGGCCAAGATCCCCACCA	2600
2451	DB	ATG	CAT	CTCTGGTGAAGACAA	CCGGT	CTCTCTGGTGTGAGGCCAAGATCCCCACCA	2510
2601	QY	CTT	CA	CCGCAAGTGGTGGGCT	CAAC	TGAGTTCCTCTCTGGTCTCTCTCTGCACTCT	2660
2511	DB	CTT	CA	CCGCAAGTGGTGGGCT	CAAC	CTGAGTTCCTCTCTGGTCTCTCTCTGCACTCT	2570
2661	QY	GGT	G	CAAAATCGTCA	CTG	ATCATCTGGTCTATACACGGGCTTCCTCCAGCTACAGGAA	2720
2571	DB	CAT	G	CAGATTGT	CAT	CTGTGTGATCTGGTCTACACGGGCCCCCTCAAGCTACGCAA	2630
2721	QY	CA	T	GAGCTGGAGGACGAGGT	CACT	CTTCACTCACTCGACGAGGGCTCGCTCATGCGCT	2780
2631	DB	CA	G	GAGCTGGAGGACGAGGT	CACT	CTTCACTCACTCGACGAGGGCTCGCTCATGCGCT	2690
2781	QY	GGG	CTT	CTCTCAT	CGGCT	TACACCTCGCTCTCGCGCCATCTGTCTTCTTCGCTTCAA	2840
2691	DB	GGG	CTT	CTCTCAT	CGGCT	TACACCTCGCTCTCGCGCCATCTGTCTTCTTCGCTTCAA	2750
2841	QY	GT	CCCGTA	AGCTCCGGAGAACTT	CA	ACGAGGCTAAGTTCATCACCTTCAGCATGTGTGAT	2900
2751	DB	GT	CCCGTA	AGCTCCGGAGAACTT	CA	ATGAAGCAAGTTCATCACCTTCAGCATGTGTGAT	2810
2901	QY	CTT	CTT	CATCGTCTGGATCT	CTT	CTTCACTCCCGCTATGTACAGCACTACGGCAAGTTGT	2960
2811	DB	CTT	CTT	CATCGTCTGGATCT	CTT	CTTCACTCTCGCTATGTACAGCACTATGGCAAGTTGT	2870
2961	QY	GT	CGGCGT	GGAGGTGAT	TGCCA	TCTTGGCTCCAGCTTCGGCTCTGGGTGCAATTA	3020
2871	DB	CT	CTGCGT	AGAGGTGAT	TGCCA	TCTTGGCAGCAGCTTGGCTTGGCTGGCTGTGCACTTT	2930
3021	QY	CTT	CA	CAAGTGTATCAT	CACT	CTGTTCAGCCGTGCGCTTAACACCATTCGAGAGTGGG	3080
2931	DB	CTT	CA	CAAGATCTATCAT	CACT	CTTCTTCAAGCCATCCCGCAACACCATTCGAGAGTGGG	2990
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2991	DB	TTG	C	AGCACCGCAGCTCAC	CGCTT	TCAAGTGGCTGCCCGGCCACCGTGGCGCGCAGCAA	3050
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3111	DB	C	A	TGAGCAAGAGCAACA	-----	GGAAAGACCATTTCCACAGCCGAGAGGCAAG	3165
3261	QY	CG	S	CAGCGGCACCGT	CAC	CTGTCTGCTTCTGAGGACAGCGGCGATACGCCACCTT	3320
3166	DB	C	A	GACGACCGCT	TGGCCCTTAA	CCGACAGAGCAGCAGCAGCGCTCGACCTCCCA	3225
3321	QY	C	A	GCGCAGCGCCG	CAGCAAG	CACTCGGCGGATGGCGGAG	3362
3226	DB	C	A	GCAAGCAAGTCT	CAGCAGCAGCC	CAAGTCAAGCAGCAAG	3267

RESULT	15
AX548832	
LOCUS	AX548832      3783 bp    DNA           linear          PAT 26-NOV-2002
DEFINITION	Sequence 117 from Patent WO02061087.
ACCESSION	AX548832
VERSION	AX548832.1 GI:25813725
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 Burmer,G.C., Roush,C.L. and Brown,J.P. Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides
AUTHORS	
TITLE	

QY 1401 CATCGGCTTCGCTCTCAGGCGGGGGCGTATCCAGGGTTCAACAGTTCTCTGAAGAGGT 1460  
 Db 1323 CATTTGATTCGCTCTGAAGGCTCGGCGAGATCCAGGCTTCGCGGAATTCCTGAAGAAGGT 1382  
 QY 1461 CCACCCAGCAGGTCCTCGACAAATGGGTTTGTCAAGGAGTTCCTGGAGAGACCTTTCAA 1520  
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 Db 1911 CTATGCCAAGAGGAGAAAGACTCTTCATCAACAGGAGAAATCTCTGAGAGTGGGT 1970  
 QY 2061 CTCCAAAGTGGTTCTTTCTCAACTGCAAGTGCAGACTGTGTCGGGGCACAGGAAGG 2120  
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 Db 2211 GATCGCATCAACCTCTTTGCGGTGTGCGGATTTTCTGACAGCTTTGTGCTGGGTGT 2270  
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Db 2391 GGACTGGACGTGCGCTCGCGCAGCGGGCTTTGGCATCAGCTTCTGCTGTCATCTC 2450  
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 Db 2631 CCAGGAGCTGGAGGATGAGATCATCTTTCATCATCTGCGAGAGGCTCCCTCATGCGGCT 2690  
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 Db 2871 CTTCTGCTGAGGTGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2930  
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 Db 3051 CGTCTCCGCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCT 3110  
 QY 3201 CACCTGCGGCGCGGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCT 3260  
 Db 3111 CATCAGCAGCAAGAGCAACA-----GCGAAGACCTTTCACAGGCCCGAGAGGCAAG 3165  
 QY 3261 CCGCAGCGGCGGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAG 3320  
 Db 3166 CAGCAGCAGCGGCTTGGGCTTAAACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3225  
 QY 3321 CAGCGCAGCGGCGGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCT 3380  
 Db 3226 CAGCAGCAACGATCTCAGCAGCGGCTTCAAGCGCTTCAAGCGCTTCAAGCGCTTCAAGCGCT 3267

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 20:20:06 ; Search time 1807 Seconds  
(without alignments)  
12009.467 Million cell updates/sec

Title: US-10-016-496-1  
Perfect score: 4134  
Sequence: 1 aattccgtgtgtcggttc.....aagggcccgacagcaacgg 4134

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues 8269772  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N Geneseq 23Sep04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4134	100.0	4134	6	Aad41631 SKCar DNA
2	4134	100.0	4134	6	Abk14910 DNA encod
3	4134	100.0	4134	6	AbL59964 Dogfish s
4	4134	100.0	4134	10	Adh10916 Shark pol
5	4134	100.0	4134	10	Aad64738 Dogfish s
6	4134	100.0	4134	12	Adi19962 Dogfish s
7	4098	99.1	4131	2	Aat89290 Dogfish s
8	1745.2	42.2	3234	2	Aaz31049 Human cal
9	1745.2	42.2	3234	2	Aax30922 Human cal
10	1745.2	42.2	3234	2	Aal43269 Human cal
11	1745.2	42.2	3237	12	Ado29824 Human GPC
12	1745.2	42.2	3783	8	Abx74489 Human cDN
13	1745.2	42.2	3783	10	Aat61382 Parathyro
14	1745.2	42.2	3809	2	Aav26964 Human par
15	1745.2	42.2	3809	2	Aat95859 Human par
16	1745.2	42.2	3809	2	Aaz25055 Human par
17	1745.2	42.2	3809	2	Aav82485 Human par
18	1745.2	42.2	3809	2	Aaz89298 Human cal
19	1745.2	42.2	3809	3	Aaf86094 Small hum
20	1745.2	42.2	3809	5	Aaf86094 Small hum
21	1745.2	42.2	3809	6	Aai72122 cDNA enco

22	1743.6	42.2	3234	3	AAZ51398 Human wil
23	1743.6	42.2	3234	10	ACA56834 Human sig
24	1743.6	42.2	3234	12	ADI56630 Human pol
25	1743.6	42.2	3361	8	ABS57393 cDNA enco
26	1738	42.0	5275	2	AAV26962 Bovine pa
27	1738	42.0	5275	2	AAT95857 Bovine pa
28	1738	42.0	5275	2	AAZ25053 Bovine pa
29	1738	42.0	5275	2	AAV82483 Bovine pa
30	1738	42.0	5275	3	AZ89296 Bovine ca
31	1738	42.0	5275	6	Aai72120 cDNA enco
32	1737.2	42.0	3237	4	AA506331 DNA encod
33	1703.6	41.2	5006	2	AAT61381 Parathyro
34	1703.6	41.2	5006	2	AAV26963 Human par
35	1703.6	41.2	5006	2	AAZ25054 Human par
36	1703.6	41.2	5006	2	AAV82484 Human par
37	1703.6	41.2	5006	3	AZ89297 Human cal
38	1703.6	41.2	5006	5	Aaf86093 Large hum
39	1703.6	41.2	5006	6	AAI72121 cDNA enco
40	1702	41.2	5006	2	AAT95858 Human par
41	1692.6	40.9	4550	12	ADO30115 Mouse GPC
42	1681.6	40.7	5046	4	AA501709 Chicken c
43	1678.2	40.6	4113	10	ABT41930 Toxicity
44	1678.2	40.6	4113	12	ADP72828 Renal tox
45	1678.2	40.6	4131	2	AAV26965 Rat kidne

## ALIGNMENTS

RESULT 1  
AAD41631  
ID AAD41631 standard; DNA; 4134 BP.

XX AAD41631;

DT 30-OCT-2002 (first entry)

DE SKCar DNA of the invention.

KW Maxine fish; fresh water; polyvalent cation sensing receptor; PVCr;

KW immune function; fat content; receptor; ds.

XX Unidentified.

XX WO200230215-A2.

XX 18-APR-2002.

XX 11-OCT-2001; 2001WO-US031625.

XX 12-OCT-2000; 2000US-00687373.

XX (AQUA-) AQUABIO PROD SCI LLC.

XX Harris HW, Russell DR, Nearing J, Betka M;

XX WPI; 2002-394428/42.

XX Growing marine fish in fresh water involves adding polyvalent cation

XX receptor modulator and feed containing sodium chloride.

XX Disclosure; Fig 14; 71pp; English.

XX The invention relates to a method for growing marine fish in fresh water.  
CC The method involves: adding at least one polyvalent cation sensing  
CC receptor (PVCr) modulator to fresh water to modulate or maintain  
CC expression and/or sensitivity of at least one PVCr in atleast one tissue;  
CC transferring the marine fish to the fresh water, modified according to  
CC the previous step; and adding feed containing NaCl to contribute to a  
CC significant increased level of the PVCr modulator in serum of the marine  
CC fish. The invention is useful for growing marine fish in freshwater e.g.  
CC mackerel, pollock, sea bass, sword fish, tuna, winter flounder and summer  
CC flounder. The marine fish cultured by the method have stronger immune





[illegible]

RESULT 2  
ABK14910  
ID ABK









Db	421	CAGAGACAGGGCTCGACAATATGGCTCAGCTTCATCTGCGCAACTCTTATTTCTTTGGGATTTACA	480
Qy	481	CTCCTCAGTCGTGTAACAATGTCTCAGGGTATGGTCCAAACCAAAGGGGCCACAGAAGAAGGA	540
Db	481	CTCCTCAGTCGTACAATGTCTCAGGGTATGGTCCAAACCAAAGGGGCCACAGAAGAAGGA	540
Qy	541	GACATCATCTGGGAGGTCCTTCCCAATACATTTGGAGTAGCCGCGCAGGATCAGGAC	600
Db	541	GACATCATCTGGGAGGTCCTTCCCAATACATTTGGAGTAGCCGCGCAGGATCAGGAC	600
Qy	601	TTAAAAATCGAGACCGGAGGGCGACAAAATGTATTTCCGTACAATTTTTCGAGGCTTCCGATGG	660
Db	601	TTAAAAATCGAGACCGGAGGGCGACAAAATGTATTTCCGTACAATTTTTCGAGGCTTCCGATGG	660
Qy	661	CTCAGGGGATGATATTTCGCAATTTGAAGAGATTAACAACAGTAGATGACTTTCTTCGCCCAAT	720
Db	661	CTCAGGGGATGATATTTCGCAATTTGAAGAGATTAACAACAGTAGATGACTTTCTTCGCCCAAT	720
Qy	721	ATCACCTCTGGGATATCCGATATTTGACACGTGTAAACACCGTGTCCAAAGGCGCTAGAGGCA	780
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Qy	781	ACATCTAGCTTTGTGGCCCGAACAATAATCGACTCGTGTGAATCTAGATGATGTTCTGTAAAC	840
Db	781	ACATCTAGCTTTGTGGCCCGAACAATAATCGACTCGTGTGAATCTAGATGATGTTCTGTAAAC	840
Qy	841	TGCTCTGACCATATCCCATCCACATAGCAGTGTGCGGGCCACCGGGTCAGGAAATCTCC	900
Db	841	TGCTCTGACCATATCCCATCCACATAGCAGTGTGCGGGCCACCGGGTCAGGAAATCTCC	900
Qy	901	ACGGCTGTGGCCAAATCTATTGGGATTAATTTTACATTCACAGGTCAGCTATGCTCTCTCG	960
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Db	961	AGCAGGCTGCTCAGCAACAAGATGAGTACNAGGCCCTTCTGAGGACCATCCCGCAATGAT	1020
Qy	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080
Db	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080
Qy	1081	ACCTGGCGCCGACGATGACTATGGCCGCCAGGCATTGACAAAGTTCCGGGAGGAGGCC	1140
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Qy	1321	CGGATCTGGCTGGCCAGCGAGGCTTGGCCAGGCTTTCGCTCATTTGCGTCCAAAGCCAGAGTAC	1380
Db	1321	CGGATCTGGCTGGCCAGCGAGGCTTGGCCAGGCTTTCGCTCATTTGCGTCCAAAGCCAGAGTAC	1380
Qy	1381	TTCCAGTGTGTGGGGGACCAATCGGCTTTGCTCTCAGGGGGGGGGGTATCCCAAGGGTTC	1440
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Qy	1441	AACAAGTTTCTGAAGGAGGTCACCCACAGAGGTCCTCGGACAAATGGGTTTGTCAAGAG	1500
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2641 CTGGTCTTCTGCACTCTGCTGCAAAATCGTCACTGCACTATCTGCTCTACACCGG 2700  
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Qy  
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3961 TTGCAACAGGAAATTAATGACTGTAACTAAACAAATTTGTTGATTTCTTAAATGCAAT 4020  
Qy  
4021 TGTAAATCAGATGTTAAATTTGTTGATTTCTTCTGACATTAAGTACCTGGAAGCAT 4080  
Db  
4021 TGTAAATCAGATGTTAAATTTGTTGATTTCTTCTGACATTAAGTACCTGGAAGCAT 4080  
Qy  
4081 AAAAAAAGGAAATTTGTTGATTTCTTCTGACATTAAGTACCTGGAAGCAT 4134  
Db  
4081 AAAAAAAGGAAATTTGTTGATTTCTTCTGACATTAAGTACCTGGAAGCAT 4134

## RESULT 4

ADH10916  
ID ADH10916 standard; DNA; 4134 BP.  
XX AC ADH10916;  
XX DT 11-MAR-2004 (first entry)  
XX DE Shark polyvalent cation sensing receptor (PVCr) - related gene.  
XX KW polyvalent cation sensing receptor; PVCr; shark; growth increase;  
XX KM mortality reduction; gene; ds.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
XX CDS 439..3522  
XX FT /\*tag= a  
XX FT /product= "Shark PVCr-related protein"  
XX FN WO2003087331-A2.  
XX PD 23-OCT-2003.  
XX PF 09-APR-2003; 2003WO-US011188.  
XX PR 11-APR-2002; 2002US-00121441.  
XX PR 18-APR-2002; 2002US-00125772.  
XX PR 18-APR-2002; 2002US-00125778.  
XX PR 18-APR-2002; 2002US-00125792.  
XX PA (VARI-) MARICAL INC.  
XX FI Harris HW, Nearing J, Betka M;  
XX DR WPI; 2003-845319/78.  
XX DR P-PSDB; ADH10917.  
XX PT New Atlantic salmon polyvalent cation-sensing receptor, PVCr,  
XX PT polypeptides useful in commercial raising of salmon and restoration of  
XX PT wild Atlantic salmon populations especially in transfer from freshwater  
XX PS to seawater.  
XX Example 1; SEQ ID NO 1; 269pp; English.

CC The invention comprises the amino acid and coding sequences of polyvalent  
 CC cation sensing receptor (PVCr) proteins from Atlantic salmon. The DNA and  
 CC protein sequences of the invention are useful in the commercial raising  
 CC of Atlantic salmon and the restoration of wild Atlantic salmon  
 CC populations, especially in the transfer from freshwater to seawater with  
 CC increased growth and reduced mortality. The present DNA sequence encodes  
 CC a shark PVCr-related protein.

XX	Sequence 4134 BP; 1028 A; 1164 C; 1019 G; 923 T; 0 U; 0 Other;	
XX	Query Match 100.0%; Score 4134; DB 10; Length 4134;	
XX	Best Local Similarity 100.0%; Pred. No. 0;	
XX	Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 AATTCGGTGTCTGGTTCAGTCCCAAGTCTCTCCAGTGCAGAAATGAGAATGGTGTGTC 60	
Db	1 AATTCGGTGTCTGGTTCAGTCCCAAGTCTCTCCAGTGCAGAAATGAGAATGGTGTGTC 60	
Qy	61 GCATTACAGGAACATGCACTACATCTGTGTTAATGAATAATGTCACTATCTGAAGGT 120	
Db	61 GCATTACAGGAACATGCACTACATCTGTGTTAATGAATAATGTCACTATCTGAAGGT 120	
Qy	121 TATTAATAATGTTTCTGCAAGGATGCTTCAAGAGAAATCAATCTGCAAGTCTTCCCAT 180	
Db	121 TATTAATAATGTTTCTGCAAGGATGCTTCAAGAGAAATCAATCTGCAAGTCTTCCCAT 180	
Qy	181 GTCAATTGATGAATTAACCTGACAAAGGATGTAAACAAATGGAACAAAGCTGAGGAC 240	
Db	181 GTCAATTGATGAATTAACCTGACAAAGGATGTAAACAAATGGAACAAAGCTGAGGAC 240	
Qy	241 GTTCAACCTTCTTGGAGATACGATCAACCTTGAAGGAGATGGAAGACTTGGAGGAA 300	
Db	241 GTTCAACCTTCTTGGAGATACGATCAACCTTGAAGGAGATGGAAGACTTGGAGGAA 300	
Qy	301 ATGGGGATTGATCTTCCAGGAGTCTGTGTTAAAGCGATCCCTCACCAATTACAAAGATA 360	
Db	301 ATGGGGATTGATCTTCCAGGAGTCTGTGTTAAAGCGATCCCTCACCAATTACAAAGATA 360	
Qy	361 GCAGAAATCTCTCAGGATCTCTGTAAACGGGCTGGGCTAGTGGCTTGGTCAAGGAA 420	
Db	361 GCAGAAATCTCTCAGGATCTCTGTAAACGGGCTGGGCTAGTGGCTTGGTCAAGGAA 420	
Qy	421 CAGAGACAGGGGTGCACAAATGCTCAGCTTCACTGCCAACTCTTATTCTTGGGATTACA 480	
Db	421 CAGAGACAGGGGTGCACAAATGCTCAGCTTCACTGCCAACTCTTATTCTTGGGATTACA 480	
Qy	481 CTCTACAGTCTACAATGTCTCAGGGTATGGTCCAAACCAAGGGCCCAAGAAAGGA 540	
Db	481 CTCTACAGTCTACAATGTCTCAGGGTATGGTCCAAACCAAGGGCCCAAGAAAGGA 540	
Qy	541 GACATCATCTGGAGGTCTCTCCCAATACACTTTGGAGTAGCCGCCCAAGGATCAGGAC 600	
Db	541 GACATCATCTGGAGGTCTCTCCCAATACACTTTGGAGTAGCCGCCCAAGGATCAGGAC 600	
Qy	601 TTAAATCGAGACCGGAGCGACAAAATGTATTTCGGTACAAATTTTCGAGGCTTCCGATGG 660	
Db	601 TTAAATCGAGACCGGAGCGACAAAATGTATTTCGGTACAAATTTTCGAGGCTTCCGATGG 660	
Qy	661 CTCAGGGGATGATATTTCGAAATGAAGAGATTAAACAGTATGACTTCTGCCCCAAT 720	
Db	661 CTCAGGGGATGATATTTCGAAATGAAGAGATTAAACAGTATGACTTCTGCCCCAAT 720	
Qy	721 ATCACCCTGGGATATCGGATATTCACAGCTGTAAACCGTGTCCAGGGCGCTAGAGGCA 780	
Db	721 ATCACCCTGGGATATCGGATATTCACAGCTGTAAACCGTGTCCAGGGCGCTAGAGGCA 780	
Qy	781 ACACCTCAGTTTGTGGCCAGAAACAAATTCGACTCGCTGAACTTAGATGAATCTGTAAAC 840	
Db	781 ACACCTCAGTTTGTGGCCAGAAACAAATTCGACTCGCTGAACTTAGATGAATCTGTAAAC 840	
Qy	841 TGCTCTGACCATATCCCATCCCAATAGCAGTGGTGGGGCAACCGGGTCAAGGATCTCC 900	
Db	841 TGCTCTGACCATATCCCATCCCAATAGCAGTGGTGGGGCAACCGGGTCAAGGATCTCC 900	

Qy	901 ACGGCTGTGGCCAACTATTATGGGATATTTTATCATTTCCACAGGTCTAGCTATGCTCTCTCG 960	
Db	901 ACGGCTGTGGCCAACTATTATGGGATATTTTATCATTTCCACAGGTCTAGCTATGCTCTCTCG 960	
Qy	961 AGCAGGTGTCTCAGCAACAAGATAGTACAAGGCTTCTCTGAGGACCAATCCCAATGAT 1020	
Db	961 AGCAGGTGTCTCAGCAACAAGATAGTACAAGGCTTCTCTGAGGACCAATCCCAATGAT 1020	
Qy	1021 GAGCAACAGGCGCCAGGATGCGCGAGATCATCAGACACTTCCAGTGGAACTCGGTGGGA 1080	
Db	1021 GAGCAACAGGCGCCAGGATGCGCGAGATCATCAGACACTTCCAGTGGAACTCGGTGGGA 1080	
Qy	1081 ACCCTGCGACCGACAGTACTATGCGCGCCAGGATTCACAAGTTCCGGGAGGAGGCC 1140	
Db	1081 ACCCTGCGACCGACAGTACTATGCGCGCCAGGATTCACAAGTTCCGGGAGGAGGCC 1140	
Qy	1141 GTTAAGAGGACATCTGTATTGATCTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200	
Db	1141 GTTAAGAGGACATCTGTATTGATCTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200	
Qy	1201 CAGTTGAGTTTCAATCGCGGACGTATCCAGAACTCTCGGCCAAGGTCTATCGTGTCTTC 1260	
Db	1201 CAGTTGAGTTTCAATCGCGGACGTATCCAGAACTCTCGGCCAAGGTCTATCGTGTCTTC 1260	
Qy	1261 TCCAAATGGCCCGACCTGAGCGCTCATCCAGAGATAGTTCCGAGAAAATCACCCGAT 1320	
Db	1261 TCCAAATGGCCCGACCTGAGCGCTCATCCAGAGATAGTTCCGAGAAAATCACCCGAT 1320	
Qy	1321 CGATCTGGCTGGCCAGCAGGCTTGGGCCAGCTCTTCGCTCATTCGCAAGCCAGAGTAC 1380	
Db	1321 CGATCTGGCTGGCCAGCAGGCTTGGGCCAGCTCTTCGCTCATTCGCAAGCCAGAGTAC 1380	
Qy	1381 TTCCAGCTGTCTGGCGGACCATCGGCTCTCGCTCTCAGGGCGGGCGTATCCAGGGTTC 1440	
Db	1381 TTCCAGCTGTCTGGCGGACCATCGGCTCTCGCTCTCAGGGCGGGCGTATCCAGGGTTC 1440	
Qy	1441 AACAAAGTCTCTGAGGAGTCTCAGCCCGCAGGCTCTCGGCAATGGGTTTCTCAAGGAG 1500	
Db	1441 AACAAAGTCTCTGAGGAGTCTCAGCCCGCAGGCTCTCGGCAATGGGTTTCTCAAGGAG 1500	
Qy	1501 TTCTGGAGGAGACCTTCAACTGCTACTTCAACGAGAAAGACCTCGACAGCTCAAGAAAT 1560	
Db	1501 TTCTGGAGGAGACCTTCAACTGCTACTTCAACGAGAAAGACCTCGACAGCTCAAGAAAT 1560	
Qy	1561 TCCAAAGTGTCTCGCAGCGACCGGGGCTCAAGGGGACGGCTCCAAAGCGGGGAACTCC 1620	
Db	1561 TCCAAAGTGTCTCGCAGCGACCGGGGCTCAAGGGGACGGCTCCAAAGCGGGGAACTCC 1620	
Qy	1621 AGACGGACAGCCCTAGCCACCCCTGCACCTGGGGAGGAGAAATCAACAGCGTGGAGAC 1680	
Db	1621 AGACGGACAGCCCTAGCCACCCCTGCACCTGGGGAGGAGAAATCAACAGCGTGGAGAC 1680	
Qy	1681 CCTACCTGATTATACACACCTGAGGATCTCTCAATGTATACGTGGCGCTACTCTCC 1740	
Db	1681 CCTACCTGATTATACACACCTGAGGATCTCTCAATGTATACGTGGCGCTACTCTCC 1740	
Qy	1741 ATTGCTCAGCCCTGCAAGACATCCACTCTTGCAAAACCGGGACGGGCTCTTTGGCAAC 1800	
Db	1741 ATTGCTCAGCCCTGCAAGACATCCACTCTTGCAAAACCGGGACGGGCTCTTTGGCAAC 1800	
Qy	1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTCGCAGGCTCTCAACCATCTGCTGCAT 1860	
Db	1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTCGCAGGCTCTCAACCATCTGCTGCAT 1860	
Qy	1861 CTGAAGTTTACCAACAGATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920	
Db	1861 CTGAAGTTTACCAACAGATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920	
Qy	1921 GGGAACTTACACCATTTCAACTGGCAGCTCTCGCAGAGGATGAATCGGGTGTGTTCCAT 1980	
Db	1921 GGGAACTTACACCATTTCAACTGGCAGCTCTCGCAGAGGATGAATCGGGTGTGTTCCAT 1980	

1981	Qy	GAGTGGGCAACTACAAACGCCTTAGCTAAGCCAGGTGAACCGATCAACATCAACAGAAAAG	2040
1981	Db	GAGTGGGCAACTACAAACGCCTTAGCTAAGCCAGGTGAACCGATCAACATCAACAGAAAAG	2040
2041	Qy	AATACTCTCGAGTGCGCTTCCTCAAAGTGGTTCCCTTTCTCCAACTCGCAGTCGAGACTGT	2100
2041	Db	AATACTCTCGAGTGCGCTTCCTCAAAGTGGTTCTCTTTCTCCAACTCGCAGTCGAGACTGT	2100
2101	Qy	GTGCCGGCACCAAGGAAGGGCATCATCGAGGGGGAGCCCACTGCTGCTTTGAATGCATG	2160
2101	Db	GTGCCGGCACCAAGGAAGGGCATCATCGAGGGGGAGCCCACTGCTGCTTTGAATGCATG	2160
2161	Qy	GCATGTGCAGAGGAGATTACGTGATGAAAAAGATGCAAGTCGATGTAACAAAGTGCCTG	2220
2161	Db	GCATGTGCAGAGGAGATTACGTGATGAAAAAGATGCAAGTCGATGTAACAAAGTGCCTG	2220
2221	Qy	AATGATTTCTGTCGAATGAGAACCAACACGTCTGATCGCCCAAGGAGATCGAGTACCTG	2280
2221	Db	AATGATTTCTGTCGAATGAGAACCAACACGTCTGATCGCCCAAGGAGATCGAGTACCTG	2280
2281	Qy	TCTGTAGACGAGACCCTTCGGGATCGCTCTGACCATCTTCGCCCTACTGGGCATCTCTGATC	2340
2281	Db	TCTGTAGACGAGACCCTTCGGGATCGCTCTGACCATCTTCGCCCTACTGGGCATCTCTGATC	2340
2341	Qy	ACCTCTCTGCTGTGGGGTCTTCATCAAGTTCAGAAACACTCCCCTCGTGAAGGCCACC	2400
2341	Db	ACCTCTCTGCTGTGGGGTCTTCATCAAGTTCAGAAACACTCCCCTCGTGAAGGCCACC	2400
2401	Qy	AACGGGAGTTGCTWACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCCAGACTCGCTC	2460
2401	Db	AACGGGAGTTGCTWACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCCAGACTCGCTC	2460
2461	Qy	ATCTTCATCGGCGAGCCACGGACTGACCTGTCCGCTCCGCCAAACOGGCGCTTTGGCATC	2520
2461	Db	ATCTTCATCGGCGAGCCACGGACTGACCTGTCCGCTCCGCCAAACOGGCGCTTTGGCATC	2520
2521	Qy	AGCTTCGTCCTGTGCATCTCCTGCATCCTGGTGAAGACCAACCGGGTGTCTGTGCTTC	2580
2521	Db	AGCTTCGTCCTGTGCATCTCCTGCATCCTGGTGAAGACCAACCGGGTGTCTGTGCTTC	2580
2581	Qy	GAGGCCAAGATCCCCACAGCTTCCACCGAAGTGGTGGGCTCAACCTGCAGTTCCTC	2640
2581	Db	GAGGCCAAGATCCCCACAGCTTCCACCGAAGTGGTGGGCTCAACCTGCAGTTCCTC	2640
2641	Qy	CTGCTCTCTCTGCACTCTCTGTCGAAATCGTCACTGCATCATCTGGCTCTACACCGCG	2700
2641	Db	CTGCTCTCTCTGCACTCTCTGTCGAAATCGTCACTGCATCATCTGGCTCTACACCGCG	2700
2701	Qy	CCTCCCTCAGCTACAGGAACCATGAGCTGGAGGAGAGTCACTTCATCACTCGCTCGAC	2760
2701	Db	CCTCCCTCAGCTACAGGAACCATGAGCTGGAGGAGAGTCACTTCATCACTCGCTCGAC	2760
2761	Qy	GAGGGCTCGCTCATGGCGCTGGGCTTCCTCATCGGGTACACCTGCTCTCTCGCGCGCATC	2820
2761	Db	GAGGGCTCGCTCATGGCGCTGGGCTTCCTCATCGGGTACACCTGCTCTCTCGCGCGCATC	2820
2821	Qy	TGCTTCTCTTCGGCTTCAAGTCGCTGCTGAAAGTCCGAGAACTTCAACGAGGCTAAGTTC	2880
2821	Db	TGCTTCTCTTCGGCTTCAAGTCGCTGCTGAAAGTCCGAGAACTTCAACGAGGCTAAGTTC	2880
2881	Qy	ATCACCTTCAGCATGTTGATCTTCTTCATCGCTGGAATCTCTTCATCCCGGCTATGTC	2940
2881	Db	ATCACCTTCAGCATGTTGATCTTCTTCATCGCTGGAATCTCTTCATCCCGGCTATGTC	2940
2941	Qy	AGCACCTACGGCAAGTTTGTCTGGCCGTGGAGGTGATTCGCAATCTCTGCTCAAGCTTC	3000
2941	Db	AGCACCTACGGCAAGTTTGTCTGGCCGTGGAGGTGATTCGCAATCTCTGCTCAAGCTTC	3000
3001	Qy	GGGCTGCTGGCTGCATTTACTTCAACAAGTGTATCATCTGTTCGAAGCGTGCCTG	3060
3001	Db	GGGCTGCTGGCTGCATTTACTTCAACAAGTGTATCATCTGTTCGAAGCGTGCCTG	3060
3061	Qy	AACACATCAGGAGGTCGCTGCAGCACCGCGGCCACCGCTTCAAGTGTGCGGCCCG	3120

[illegible]





1261	Db	 TCCAAATGGCCCCGACCTTGGAGCGCCTCATCCAGGAGATAGTTCCGGAAACAATCATCCGAT	1320
1321	Qy	CGGATCTGGCTGGCCACGAGAGGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380
1321	Db	CGGATCTGGCTGGCCACGAGAGGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380
1381	Qy	TTCCACGTGTCTGGCGGCAACATCGGCTTCGCTCTCAGGGCGGGGCTATCCCAGGGTTC	1440
1381	Db	TTCCACGTGTCTGGCGGCAACATCGGCTTCGCTCTCAGGGCGGGGCTATCCCAGGGTTC	1440
1441	Qy	AACAAGTTCTGAAGAGGTCACCCACGAGGTCTTCGGACAATGGTTTGTCAAGGAG	1500
1441	Db	AACAAGTTCTGAAGAGGTCACCCACGAGGTCTTCGGACAATGGTTTGTCAAGGAG	1500
1501	Qy	TTCTGGAGGAGACCTTCAACTGCTACTTCAACCGAGAAGACCTCGACGCTGAAGAAT	1560
1501	Db	TTCTGGAGGAGACCTTCAACTGCTACTTCAACCGAGAAGACCTCGACGCTGAAGAAT	1560
1561	Qy	TCCAAGTGCCTCGCACGACCGCGGCTCAGGGGACGGCTCCAAGCGGGGAACCTCC	1620
1561	Db	TCCAAGTGCCTCGCACGACCGCGGCTCAGGGGACGGCTCCAAGCGGGGAACCTCC	1620
1621	Qy	AGACGACAGCCCTACGCCACCCCTGCACCTGGGGAGGAGAAATCACACGCTGGAGACC	1680
1621	Db	AGACGACAGCCCTACGCCACCCCTGCACCTGGGGAGGAGAAATCACACGCTGGAGACC	1680
1681	Qy	CCCTACTGGATTATACACACTGAGGATCTCTCAATGATATACGTGGCGCTCTACTCC	1740
1681	Db	CCCTACTGGATTATACACACTGAGGATCTCTCAATGATATACGTGGCGCTCTACTCC	1740
1741	Qy	ATTGCTCACGCCCTGCAAGACATCACTCTTGCAAAACCGGCACGGGCACTTTTGCAAC	1800
1741	Db	ATTGCTCACGCCCTGCAAGACATCACTCTTGCAAAACCGGCACGGGCACTTTTGCAAC	1800
1801	Qy	GGATCTTGTGCAGATATATAAAAGTTGAGCCTGCGAGCTCTCAACCACTGCTGCAT	1860
1801	Db	GGATCTTGTGCAGATATATAAAAGTTGAGCCTGCGAGCTCTCAACCACTGCTGCAT	1860
1861	Qy	CTGAGTTTACCAACGACATGGGTGAGCGATTGACTTTGACGATCAAGTGACCTCAAG	1920
1861	Db	CTGAGTTTACCAACGACATGGGTGAGCGATTGACTTTGACGATCAAGTGACCTCAAG	1920
1921	Qy	GGAACTTACACCATTTCAACTGGCAGCTCTCCGACAGAGATGAATCGGTGTTGTTCCAT	1980
1921	Db	GGAACTTACACCATTTCAACTGGCAGCTCTCCGACAGAGATGAATCGGTGTTGTTCCAT	1980
1981	Qy	GAGTGGGCAACTACAACGCTTACCTAAGCCAGTGAACCGACTCAACATCAACGAAAG	2040
1981	Db	GAGTGGGCAACTACAACGCTTACCTAAGCCAGTGAACCGACTCAACATCAACGAAAG	2040
2041	Qy	AAATCTCTTGGAGTGGCTTCTCCAAAGTGGTTCTTCTTCCAACTGCACTCGAGTGT	2100
2041	Db	AAATCTCTTGGAGTGGCTTCTCCAAAGTGGTTCTTCTTCCAACTGCACTCGAGTGT	2100
2101	Qy	GTCCCGGGCAACAGGAAGGGGATCATCGAGGGGAGCCCACTGCTGCTTTGATGCTATG	2160
2101	Db	GTCCCGGGCAACAGGAAGGGGATCATCGAGGGGAGCCCACTGCTGCTTTGATGCTATG	2160
2161	Qy	GCATGTGACAGGAGGAGTTTCAGTGATGAAAACGATGCAAGTCCGTGTACAAGTCCCG	2220
2161	Db	GCATGTGACAGGAGGAGTTTCAGTGATGAAAACGATGCAAGTCCGTGTACAAGTCCCG	2220
2221	Qy	AATGATTTCTGTGCGAATGAGAACCAACGTCGTGATCGCCAAGGAGATCGAGTACCTG	2280
2221	Db	AATGATTTCTGTGCGAATGAGAACCAACGTCGTGATCGCCAAGGAGATCGAGTACCTG	2280
2281	Qy	TGCTGACGAGGCCCTTCGGGATCGCTCTGACCATCTTCGCGTACTGGGCATCCTGATC	2340
2281	Db	TGCTGACGAGGCCCTTCGGGATCGCTCTGACCATCTTCGCGGATCTGGGCATCCTGATC	2340
2341	Qy	ACCTCCTCTGCTGGGGGTCTTTCATCAAGTTTCAGGAAACATCTCCCATCGTAGGGCCACC	2400

PR	12-OCT-2000; 2000US-00687476.
PR	12-OCT-2000; 2000US-00687477.
PR	11-OCT-2001; 2001US-00975553.
PR	11-OCT-2001; 2001WO-US031562.
XX	(MARI-) MARICAL INC.
XX	Harris HW, Russell DR, Nearing J, Betka M;
PI	WPI; 2004-061122/06.
DR	P-PSDB; ADI19970.
XX	Growing pre-adult anadromous fish in freshwater comprises adding feed
PT	containing an amount of NaCl for fish consumption to the freshwater to
PT	increase the level of the Polyvalent Cation Sensing Receptor modulator in
PT	serum of the fish.
XX	Example 19; SEQ ID NO 17; 109pp; English.
XX	The present invention relates to methods for improving the raising of pre-
CC	-adult anadromous fish or preparing these fish for transfer to seawater
CC	by modulating expression of a receptor referred to as the Polyvalent
CC	Cation Sensing Receptor (PVCr). The invention is useful in increasing
CC	survival and growth and reduce stress of the fish that have been
CC	transferred to seawater. The present sequence is a dogfish shark cation
CC	receptor (SKCaR) DNA.
XX	Sequence 4134 BP; 1028 A; 1164 C; 1019 G; 923 T; 0 U; 0 Other;
SQ	
	Query Match 100.0%; Score 4134; DB 12; Length 4134;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 AATTCGGTGTGCTCGGGTTCCAGTGCCAAAGTCTCCTCCAGTGCAAAATGAGAAATGGTGTC 60
Db	1 AATTCGGTGTGCTCGGGTTCCAGTGCCAAAGTCTCCTCCAGTGCAAAATGAGAAATGGTGTC 60
QY	61 GCCATTACAGAACATGCATCATCTGTGTTAATGAATAATATGTCAAGTTATCTGAAGGT 120
Db	61 GCCATTACAGAACATGCATCATCTGTGTTAATGAATAATATGTCAAGTTATCTGAAGGT 120
QY	121 TATTAATAATGTTTTCTGCAAGATGGCTTCACGAGAAATCAATTCGACGTTTTCCCATT 180
Db	121 TATTAATAATGTTTTCTGCAAGATGGCTTCACGAGAAATCAATTCGACGTTTTCCCATT 180
QY	181 GTCATTTGTGAATAACTGCCAAAAGGATGTAAACAAATGGAAACAAGCTGAGACCAC 240
Db	181 GTCATTTGTGAATAACTGCCAAAAGGATGTAAACAAATGGAAACAAGCTGAGACCAC 240
QY	241 GTTCACCCCTTCTTGGAGCATACGATCACCCCTGAGGAGATGGAAGACTTGAGAGGAA 300
Db	241 GTTCACCCCTTCTTGGAGCATACGATCACCCCTGAGGAGATGGAAGACTTGAGAGGAA 300
QY	301 ATGGGAGTTGATCTTCACGAGTTCTGCTGTAAAGCGATCCCTCACCATTAACAAGATAA 360
Db	301 ATGGGAGTTGATCTTCACGAGTTCTGCTGTAAAGCGATCCCTCACCATTAACAAGATAA 360
QY	361 GCAGAAATCTCTCAGGCATCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420
Db	361 GCAGAAATCTCTCAGGCATCTCTGTAAACGGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420
QY	421 CAGAGACAGGCTGCACAAATGGCTCAGCTTCACTGCGCAACTCTTATCTTGGGATTTACA 480
Db	421 CAGAGACAGGCTGCACAAATGGCTCAGCTTCACTGCGCAACTCTTATCTTGGGATTTACA 480
QY	481 CTCCTACAGTCGTACAATGTCTCAGSGTATGFTCCAAACCAAAGGGCCAGAGAAGGA 540
Db	481 CTCCTACAGTCGTACAATGTCTCAGSGTATGFTCCAAACCAAAGGGCCAGAGAAGGA 540
QY	541 GACATCATCTGCGAGGTCTCTTCCCAATACATTTTGGAGTAGTCGCCCAAGGATCAGCAC 600
Db	541 GACATCATCTGCGAGGTCTCTTCCCAATACATTTTGGAGTAGTCGCCCAAGGATCAGCAC 600

Qy 601 TTAATAATCGAGACCGGAGCGCAAAATGTATTCGGTACAATTTTCGAGGCTTCGATGG 660  
Db 601 TTAATAATCGAGACCGGAGCGCAAAATGTATTCGGTACAATTTTCGAGGCTTCGATGG 660  
Qy 661 CTCAGGCGGATGATATTCGCAATTGAAGAGATTAAACAAGTATGACTTTCCTGCCCAAT 720  
Db 661 CTCAGGCGGATGATATTCGCAATTGAAGAGATTAAACAAGTATGACTTTCCTGCCCAAT 720  
Qy 721 ATCACCCTGGGATATCGCATATTTGACAGCTGTAAACACCGTTCGCAAGCGCTAGAGCA 780  
Db 721 ATCACCCTGGGATATCGCATATTTGACAGCTGTAAACACCGTTCGCAAGCGCTAGAGCA 780  
Qy 781 ACACCTCAGCTTTGTGGCCCGAGACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAA 840  
Db 781 ACACCTCAGCTTTGTGGCCCGAGACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAA 840  
Qy 841 TGTCTGACCATATCCCATCCCAATAGCAGTGGTTCGGGCAACCGGTCAGGAATCTCC 900  
Db 841 TGTCTGACCATATCCCATCCCAATAGCAGTGGTTCGGGCAACCGGTCAGGAATCTCC 900  
Qy 901 ACGGCTGTGGCCCAATCTATTTGGATTTATTTTACATTCGACAGGTGATGCTCTCTCG 960  
Db 901 ACGGCTGTGGCCCAATCTATTTGGATTTATTTTACATTCGACAGGTGATGCTCTCTCG 960  
Qy 961 AGCAGGCTGTGACCAACAGAAATAGTACAAAGGCTTCCTGAGGACCATCCCAATGAT 1020  
Db 961 AGCAGGCTGTGACCAACAGAAATAGTACAAAGGCTTCCTGAGGACCATCCCAATGAT 1020  
Qy 1021 GAGCAACAGGCCACCGCCATGCGGAGATCATCGAGCACTTCAGTGGAACTTGGTGGGA 1080  
Db 1021 GAGCAACAGGCCACCGCCATGCGGAGATCATCGAGCACTTCAGTGGAACTTGGTGGGA 1080  
Qy 1081 ACCCTGGAGCGACGATGACTATGCGCGCCGAGGATTTGACAGTTCCGGGAGGAGGCC 1140  
Db 1081 ACCCTGGAGCGACGATGACTATGCGCGCCGAGGATTTGACAGTTCCGGGAGGAGGCC 1140  
Qy 1141 GTTAAGAGGAGACATCTGTATTTGACTTCAGTGAGATGATCTCTCAGTACTACACCGAAG 1200  
Db 1141 GTTAAGAGGAGACATCTGTATTTGACTTCAGTGAGATGATCTCTCAGTACTACACCGAAG 1200  
Qy 1201 CAGTTGGAGTTGATCGCGAGCTATCCAGAACTCTCGGCCAAGGTCACTGGTCTTTC 1260  
Db 1201 CAGTTGGAGTTGATCGCGAGCTATCCAGAACTCTCGGCCAAGGTCACTGGTCTTTC 1260  
Qy 1261 TCCAAATGGCCCCGACCTGAGCGGCTCATCCAGGAGATAGTTCCGGAGAAACATACCGAT 1320  
Db 1261 TCCAAATGGCCCCGACCTGAGCGGCTCATCCAGGAGATAGTTCCGGAGAAACATACCGAT 1320  
Qy 1321 CGGATCTGGTGGCCAGCGAGGTTGGGCCAGCTCTTCGCTCATTTGCCAAGCCAGATAC 1380  
Db 1321 CGGATCTGGTGGCCAGCGAGGTTGGGCCAGCTCTTCGCTCATTTGCCAAGCCAGATAC 1380  
Qy 1381 TTCCAGTGGTGGCGGACCACTGCGCTTCGCTCTCAGGCGGCGGTATCCAGGGTTC 1440  
Db 1381 TTCCAGTGGTGGCGGACCACTGCGCTTCGCTCTCAGGCGGCGGTATCCAGGGTTC 1440  
Qy 1441 AACAAAGTTCTGAAGAGTTCACCCAGAGGCTCTCGGACAAATGGGTTGTCAAGAG 1500  
Db 1441 AACAAAGTTCTGAAGAGTTCACCCAGAGGCTCTCGGACAAATGGGTTGTCAAGAG 1500  
Qy 1501 TTCTGGGAGAGACTTCAACTGCTACTTCAACGAGAGACCTGACGAGCTGAGAT 1560  
Db 1501 TTCTGGGAGAGACTTCAACTGCTACTTCAACGAGAGACCTGACGAGCTGAGAT 1560  
Qy 1561 TCCAAAGTGGCTTCGACCGGACCGGCTCAAGGGGACGGTCCAAAGCGGGAACTCC 1620  
Db 1561 TCCAAAGTGGCTTCGACCGGACCGGCTCAAGGGGACGGTCCAAAGCGGGAACTCC 1620  
Qy 1621 AGACGAGACGCTTACGCCACCCCTGCACTGGGAGGAGAACATCAGAGGTGAGAGC 1680  
Db 1621 AGACGAGACGCTTACGCCACCCCTGCACTGGGAGGAGAACATCAGAGGTGAGAGC 1680  
Qy 1681 CCTACTCGGATTAATACACCTGAGGATCTCTCAATGTATAGCTGGCGCTCTACTCC 1740

Db 1681 CCCTACTCGGATTAATACACACCTGAGGATCTCTCAATGTATACGTGGCGCTCTACTCC 1740  
Qy 1741 ATTCTCACCCTCTGAAGACATCCACTCTTGCAAAACCCGGCACGGGCATCTTTGCAAAAC 1800  
Db 1741 ATTCTCACCCTCTGAAGACATCCACTCTTGCAAAACCCGGCACGGGCATCTTTGCAAAAC 1800  
Qy 1801 GGATCTTTGTGAGATATATAAAAGTTGAGGCTCTGGCAGGTCTCTCAACATCTGCTGCAT 1860  
Db 1801 GGATCTTTGTGAGATATATAAAAGTTGAGGCTCTGGCAGGTCTCTCAACATCTGCTGCAT 1860  
Qy 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGTTGACTTTTCAACGATCAAGGTGACCTCAAG 1920  
Db 1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGTTGACTTTTCAACGATCAAGGTGACCTCAAG 1920  
Qy 1921 GGGAACTACACCATTTATCAAATGCGAGCTCTCGCAGAGGATGAATCGGTGTTGTTCAT 1980  
Db 1921 GGGAACTACACCATTTATCAAATGCGAGCTCTCGCAGAGGATGAATCGGTGTTGTTCAT 1980  
Qy 1981 GAGGTGGCAACTACACGCTAGCGTTAGCCCGCAGTGACCGACTCAACATCAACGAAAG 2040  
Db 1981 GAGGTGGCAACTACACGCTAGCGTTAGCCCGCAGTGACCGACTCAACATCAACGAAAG 2040  
Qy 2041 AAAATCCTCTGAGTGGCTTTCTCAAAGTGGTTCTTTCTCCTCAACTGCGAGTGGTCTGT 2100  
Db 2041 AAAATCCTCTGAGTGGCTTTCTCAAAGTGGTTCTTTCTCCTCAACTGCGAGTGGTCTGT 2100  
Qy 2101 GTGCGGGCAACAGGAGGATCATCGAGGGGAGGCCACCTGCTGCTTGAATGATG 2160  
Db 2101 GTGCGGGCAACAGGAGGATCATCGAGGGGAGGCCACCTGCTGCTTGAATGATG 2160  
Qy 2161 GCATGTGCAGAGGAGATTCAGTGTGAAACGATGCAAGTGCCTGTGTAACAAAGTGGCCG 2220  
Db 2161 GCATGTGCAGAGGAGATTCAGTGTGAAACGATGCAAGTGCCTGTGTAACAAAGTGGCCG 2220  
Qy 2221 AATGATTTCTGTCGAATGAGAACCAAGCTGTGATCGCCAAAGGAGATCGAGTACCTG 2280  
Db 2221 AATGATTTCTGTCGAATGAGAACCAAGCTGTGATCGCCAAAGGAGATCGAGTACCTG 2280  
Qy 2281 TCGTGGAGGAGCCCTTCGGGATCGCTGACCATCTTCGCGCTACTGGGCATCTCTGATC 2340  
Db 2281 TCGTGGAGGAGCCCTTCGGGATCGCTGACCATCTTCGCGCTACTGGGCATCTCTGATC 2340  
Qy 2341 ACCTCTCTGCTGCTGGGGTCTTCATCAAGTTTCAGGAACAATCCCATCGTGAAGGCCACC 2400  
Db 2341 ACCTCTCTGCTGCTGGGGTCTTCATCAAGTTTCAGGAACAATCCCATCGTGAAGGCCACC 2400  
Qy 2401 AACGGGAGTTGCTTACCTGCTGCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460  
Db 2401 AACGGGAGTTGCTTACCTGCTGCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460  
Qy 2461 ATCTTCATCGCGAGCCAGGAGCTGGAACCTGCGCTCGGCCAACCGGCCCTTTGSCATC 2520  
Db 2461 ATCTTCATCGCGAGCCAGGAGCTGGAACCTGCGCTCGGCCAACCGGCCCTTTGSCATC 2520  
Qy 2521 AGCTTCGCTCTGTCATCTCTGTCATCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTC 2580  
Db 2521 AGCTTCGCTCTGTCATCTCTGTCATCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTC 2580  
Qy 2581 GAGGCCAAGATCCCAACAGCCCTCCAGCAAGTGGTGGGCTCAACCTGCAAGTTCTTC 2640  
Db 2581 GAGGCCAAGATCCCAACAGCCCTCCAGCAAGTGGTGGGCTCAACCTGCAAGTTCTTC 2640  
Qy 2641 CTGGTCTTCTCTGTCATCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2700  
Db 2641 CTGGTCTTCTCTGTCATCTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 2700  
Qy 2701 CCTCCCTCCAGCTTACAGGACCATGAGCTGGAGGAGGATCATCTTTCATCTCCTCGAC 2760  
Db 2701 CCTCCCTCCAGCTTACAGGACCATGAGCTGGAGGAGGATCATCTTTCATCTCCTCGAC 2760  
Qy 2761 GAGGGCTCGCTCATGCGCTGGGCTTCTCATCGGCTACACCTGCTCTCGCGGCTC 2820

Db 2761 GAGGGCTCGCTCATGGCGCTGGGCTTCTCTATCGGCTACACCTGCGCTCTCGCGCCATC 2820  
Qy 2821 TGCCTCTCTTCTCGCTTCAAGTCCCGTAAAGCTGCGGAGAACTTCAACGAGGCTAAGTTC 2880  
Db 2821 TGCCTCTCTTCTCGCTTCAAGTCCCGTAAAGCTGCGGAGAACTTCAACGAGGCTAAGTTC 2880  
Qy 2881 ATCAGCTTCAGCATGTGATCTTCTTCATCGTCTGATCTCTCTCATCCCGCTATGTC 2940  
Db 2881 ATCAGCTTCAGCATGTGATCTTCTTCATCGTCTGATCTCTCTCATCCCGCTATGTC 2940  
Qy 2941 AGCACTAGCGAAGTTTGTGTCGCGTGGAGGTGATTCATCCTCGCTCCAGCTTC 3000  
Db 2941 AGCACTAGCGAAGTTTGTGTCGCGTGGAGGTGATTCATCCTCGCTCCAGCTTC 3000  
Qy 3001 GGCTGCTGGCTGCTGCTTCAACAGTGTATCATCATCTCTGTCAAGCGCTGCGGT 3060  
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Qy 3061 AACACCATGAGAGTGGCTGACAGCGGCGGCCACGCTTCAAGGTGGCGGCCGG 3120  
Db 3061 AACACCATGAGAGTGGCTGACAGCGGCGGCCACGCTTCAAGGTGGCGGCCGG 3120  
Qy 3121 GCCACCTCCGCGCAGCGCCGCTCTCGCAAGCGCTCCAGCAGCTGTGCGGCTCCACC 3180  
Db 3121 GCCACCTCCGCGCAGCGCCGCTCTCGCAAGCGCTCCAGCAGCTGTGCGGCTCCACC 3180  
Qy 3181 ATCTCTCTCGCGCTCGTCCACCTGCGGCGCGGCTTCAACAGTGTGAGTGTGCTGC 3240  
Db 3181 ATCTCTCTCGCGCTCGTCCACCTGCGGCGCGGCTTCAACAGTGTGAGTGTGCTGC 3240  
Qy 3241 AGCAGCAGAGGTGAGTTCGCGCAGCGCAGCTCACCTCTGCTGAGCTTCAGAG 3300  
Db 3241 AGCAGCAGAGGTGAGTTCGCGCAGCGCAGCTCACCTCTGCTGAGCTTCAGAG 3300  
Qy 3301 ACAGGCGGATAGCCACCTCTAGCGCGCAGCGCGCAGCAGAACTCGCGGATGCGCG 3360  
Db 3301 ACAGGCGGATAGCCACCTCTAGCGCGCAGCGCGCAGCAGAACTCGCGGATGCGCG 3360  
Qy 3361 AGCGGCGAGCTGCTGCTATGACACACGAGCGCGCGCTCAGAAATGCGAGCGC 3420  
Db 3361 AGCGGCGAGCTGCTGCTATGACACACGAGCGCGCGCTCAGAAATGCGAGCGC 3420  
Qy 3421 CAGCGCGCAACGATCCCGATACAGGCGCGCGCAGCAAGGCACTTAGAGTTCGCG 3480  
Db 3421 CAGCGCGCAACGATCCCGATACAGGCGCGCGCAGCAAGGCACTTAGAGTTCGCG 3480  
Qy 3481 GCGGCGAGAGAGCGCGCCCAACTATGAGGAGAACTTAATCCAACTCTCCATCAAC 3540  
Db 3481 GCGGCGAGAGAGCGCGCCCAACTATGAGGAGAACTTAATCCAACTCTCCATCAAC 3540  
Qy 3541 CCCAAGACATCTCCACGCGCAGCGTCCGCACTGACATCACTCTTAACCGTGGC 3600  
Db 3541 CCCAAGACATCTCCACGCGCAGCGTCCGCACTGACATCACTCTTAACCGTGGC 3600  
Qy 3601 TGCCCAACCTCTCCCTCTCGGCACTTTGCGTTTGTGAGGATTCGAGCTTCGAGT 3660  
Db 3601 TGCCCAACCTCTCCCTCTCGGCACTTTGCGTTTGTGAGGATTCGAGCTTCGAGT 3660  
Qy 3661 TCCTTTATCCCTGATTTCTGACTTGGATTTTACTAGTTCGATGGAATATCAAC 3720  
Db 3661 TCCTTTATCCCTGATTTCTGACTTGGATTTTACTAGTTCGATGGAATATCAAC 3720  
Qy 3721 ATATGAGTTGCAATTTAGTTCAGCAGAGTTCGTCAAAGTATCTGAATCTCTGAAGT 3780  
Db 3721 ATATGAGTTGCAATTTAGTTCAGCAGAGTTCGTCAAAGTATCTGAATCTCTGAAGT 3780  
Qy 3781 ATCTGAATCTTATTTCTCGAATGTATTAACAACATTTGAAGTATTTTAGTGACA 3840  
Db 3781 ATCTGAATCTTATTTCTCGAATGTATTAACAACATTTGAAGTATTTTAGTGACA 3840  
Qy 3841 TTATGTTCTAACATTTCTGAGATAATTTGTTACACATATATAGGATCCACCTGAAGCACT 3900  
Db 3841 TTATGTTCTAACATTTCTGAGATAATTTGTTACACATATATAGGATCCACCTGAAGCACT 3900

Qy 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATAACATTTATCAATGAAACCTGGA 3960  
Db 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATAACATTTATCAATGAAACCTGGA 3960  
Qy 3961 TTGCAACAGGAATATANTGACTGTACAAAAAATTTGTTGATTATCTTAAAAATGCAAT 4020  
Db 3961 TTGCAACAGGAATATANTGACTGTACAAAAAATTTGTTGATTATCTTAAAAATGCAAT 4020  
Qy 4021 TGTAATCAGATGTGTAATAATTTGTTAAATTTCTGTAACATTAATGATATTTCTTGATA 4080  
Db 4021 TGTAATCAGATGTGTAATAATTTGTTAAATTTCTGTAACATTAATGATATTTCTTGATA 4080  
Qy 4081 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 4134  
Db 4081 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA 4134

## RESULT 7

AAT89290  
ID AAT89290 standard; cDNA; 4131 bp.

AC AAT89290;

XX 27-MAR-1998 (first entry)

XX Dogfish shark kidney calcium receptor related protein cDNA.

XX Calcium receptor related protein; Car-RP; dogfish shark; SKCaR-RP;

KW polycation-sensing receptor; aquaculture; fish farming;

XX salinity tolerance; ss.

OS Squalus acanthias.

XX Key Location/Qualifiers

PH 439..3519

FT /\*tag= a

FT polyA\_site 4076..4113

FT /\*tag= b

XX WO9735977-A1.

XX 02-OCT-1997.

XX 27-MAR-1997; 97WO-US005031.

XX 27-MAR-1996; 96US-00622738.

XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.

XX Harris HW, Brown E, Hebert S;

XX WPI; 1997-489640/45.

XX P-PsDB; AAW32059.

XX New isolated Aquatic polyvalent cation-sensing receptor - used to develop products for increasing or decreasing the salinity tolerance of fish for use in aquaculture.

XX Claim 2; Fig 4A-F; 57pp; English.

XX This cDNA clone codes for dogfish shark kidney calcium receptor related protein (SKCaR-RP, see AAW32059), an aquatic polyvalent cation-sensing receptor (pVCR). It was isolated from a shark kidney cDNA library using a rat kidney calcium receptor cDNA as probe. Also claimed are: a probe comprising the 4131 bp SKCaR-RP sequence; an isolated pVCR present in the plasma membranes of aquatic species, especially on the apical membrane of epithelial cells of elasmobranch fish, particularly from cells found in the collecting duct or late distal tubule in the kidney, intestine, gall, rectal gland, gonad or brain; an antibody that specifically binds to a pVCR; and a method of screening for aquatic pVCR agonists and antagonists. Modulation of the expression of the aquatic pVCR activates or inhibits aquatic pVCR mediated ion transport and endocrine changes

CC that permit fish to adapt to fresh or salt water. The method facilitates  
 CC the aquaculture of marine fish and can provide for the development of  
 CC marine fish that are easily adaptable to fresh water aquaculture  
 XX

SQ Sequence 4131 BP; 1028 A; 1161 C; 1019 G; 923 T; 0 U; 0 Other;

Query Match 99.1%; Score 4098; DB 2; Length 4131;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 4131; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY	1	AATTCGGTGTCTCGGTTTCAGTCCAAAGTCTCTCCAGTGCAGAAATGAGAAATGGTGGTC	60
DB	1	AATTCGGTGTCTCGGTTTCAGTCCAAAGTCTCTCCAGTGCAGAAATGAGAAATGGTGGTC	60
QY	61	GCATTACAGGAACATGCATCATCTGTGTTAATGAAATATGTTCAGTTATCTGAAGT	120
DB	61	GCATTACAGGAACATGCATCATCTGTGTTAATGAAATATGTTCAGTTATCTGAAGT	120
QY	121	TATTAATAATGTTTCTGCAAGATGGCTTCACAGAAATCAATCTGCAGCTTTTCCCAT	180
DB	121	TATTAATAATGTTTCTGCAAGATGGCTTCACAGAAATCAATCTGCAGCTTTTCCCAT	180
QY	181	GTCAATGTATGAATACTGACCAAGGGATGTAACAAATGGAACAAAGCTGAGGACAC	240
DB	181	GTCAATGTATGAATACTGACCAAGGGATGTAACAAATGGAACAAAGCTGAGGACAC	240
QY	241	GTTACCCCTTCTTGAGCATACGATCAACCTCGAGGAGATGGAAGCTTCAGAGGAA	300
DB	241	GTTACCCCTTCTTGAGCATACGATCAACCTCGAGGAGATGGAAGCTTCAGAGGAA	300
QY	301	ATGGGATGTATCTCCAGAGTTCTGCTGTAAGCGATCCCTCAACATTAACAAGATAA	360
DB	301	ATGGGATGTATCTCCAGAGTTCTGCTGTAAGCGATCCCTCAACATTAACAAGATAA	360
QY	361	GCAGAAATCTCCAGGATCTCTGTAAACGGGCTGGCTAGTGGTGTGTCAGGAA	420
DB	361	GCAGAAATCTCCAGGATCTCTGTGTAAACGGGCTGGCTAGTGGTGTGTCAGGAA	420
QY	421	CAGAGACAGGCTGCACATGGCTCAGCTTCACTGCAACCTCTTATCTTGGGATTTACA	480
DB	421	CAGAGACAGGCTGCACATGGCTCAGCTTCACTGCAACCTCTTATCTTGGGATTTACA	480
QY	481	CTCCTACAGTGTGAATGTCTCAGGGTATGTTCCAAACCAAGGCGCCAGAAAGGA	540
DB	481	CTCCTACAGTGTGAATGTCTCAGGGTATGTTCCAAACCAAGGCGCCAGAAAGGA	540
QY	541	GACATCATCTGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAGAGTCAAGAC	600
DB	541	GACATCATCTGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAGAGTCAAGAC	600
QY	601	TAAATACAGACCGGAGCGCAAAATGTATTCGGTACAAATTTTCGAGGCTTCGATGG	660
DB	601	TAAATACAGACCGGAGCGCAAAATGTATTCGGTACAAATTTTCGAGGCTTCGATGG	660
QY	661	CTCCAGGCTGATATTCGCAATGAGAGATTAACACAGTATGATCTTCTGCGCCCAAT	720
DB	661	CTCCAGGCTGATATTCGCAATGAGAGATTAACACAGTATGATCTTCTGCGCCCAAT	720
QY	721	ATCACCTCTGGGATATCGCATATTTGACACGTGTAAACCGTGTCCAAAGCGCTAGAGGA	780
DB	721	ATCACCTCTGGGATATCGCATATTTGACACGTGTAAACCGTGTCCAAAGCGCTAGAGGA	780
QY	781	ACACTCAGCTTTGTGGCCAGAACAAATCGATCGCTGAACTTAGATGATTTCTGTAAC	840
DB	781	ACACTCAGCTTTGTGGCCAGAACAAATCGATCGCTGAACTTAGATGATTTCTGTAAC	840
QY	841	TGCTCTGACCATATCCATCCCAATAGCAGTGGTGGGGCAACCGGGTCAGGAATCTCC	900
DB	841	TGCTCTGACCATATCCATCCCAATAGCAGTGGTGGGGCAACCGGGTCAGGAATCTCC	900
QY	901	ACGGTGTGGCCAAATCTATTTGGAATTTATTTTACATTCACAGGTGAGCTATGCTTCG	960
DB	901	ACGGTGTGGCCAAATCTATTTGGAATTTATTTTACATTCACAGGTGAGCTATGCTTCG	960

QY	961	AGCAGGCTGTCTACGAAACAAGATGAGTACAAGGCTTCTCTGAGGACCATCCCAATGAT	1020
DB	961	AGCAGGCTGTCTACGAAACAAGATGAGTACAAGGCTTCTCTGAGGACCATCCCAATGAT	1020
QY	1021	GAGCAACAGGCGACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGTGGGA	1080
DB	1021	GAGCAACAGGCGACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGTGGGA	1080
QY	1081	ACCCTGACGCGCAGATGACTATGGCCGCCAGGCAATGACAAGTTCCGGGAGGAGGCC	1140
DB	1081	ACCCTGACGCGCAGATGACTATGGCCGCCAGGCAATGACAAGTTCCGGGAGGAGGCC	1140
QY	1141	GTTAAGAGGACATCTGTATTTGACTTCAGTGAGATGATCTCTCAGTACTACCCAGAAG	1200
DB	1141	GTTAAGAGGACATCTGTATTTGACTTCAGTGAGATGATCTCTCAGTACTACCCAGAAG	1200
QY	1201	CAGTTGAGTTTCATCGCCGACGTCATCCAGAACTCTCTCGGCCAAGTTCATCTGTTCTTC	1260
DB	1201	CAGTTGAGTTTCATCGCCGACGTCATCCAGAACTCTCTCGGCCAAGTTCATCTGTTCTTC	1260
QY	1261	TCCAAATGGCCCGACCTTGGAGCGCTCATCCAGAGATAGTTCCGAGAAACATCCCGAT	1320
DB	1261	TCCAAATGGCCCGACCTTGGAGCGCTCATCCAGAGATAGTTCCGAGAAACATCCCGAT	1320
QY	1321	CGGATCTGGCTGGCCAGGAGGCTTGGCCAGCTCTTTCGCTCATTTGCCAAGCCAGAGTAC	1380
DB	1321	CGGATCTGGCTGGCCAGGAGGCTTGGCCAGCTCTTTCGCTCATTTGCCAAGCCAGAGTAC	1380
QY	1381	TTCCACCTGTGGCGGCAACATCGCTTCTCAGGGCGGGCTATCCAGGGTTC	1440
DB	1381	TTCCACCTGTGGCGGCAACATCGCTTCTCAGGGCGGGCTATCCAGGGTTC	1440
QY	1441	AACAAGTTCTGAGGAGGCTCCACCCAGCAGGCTCTCGGACAAATGGTTTGTCAAGGAG	1500
DB	1441	AACAAGTTCTGAGGAGGCTCCACCCAGCAGGCTCTCGGACAAATGGTTTGTCAAGGAG	1500
QY	1501	TTCTGGAGGAGACCTTTCAACTGCTACTTCAACCGAGAGAACCTGACGAGCTGGAAGAT	1560
DB	1501	TTCTGGAGGAGACCTTTCAACTGCTACTTCAACCGAGAGAACCTGACGAGCTGGAAGAT	1560
QY	1561	TCCAGGTGCTCTCGACGACCGGGCTCTAGGGGACGGCTCCAAAGCGGGGAACTCC	1620
DB	1561	TCCAGGTGCTCTCGACGACCGGGCTCTAGGGGACGGCTCCAAAGCGGGGAACTCC	1620
QY	1621	AGACGACAGCCCTTACGCCACCCCTGCACTGGGGAGGAGAACATCACACGCTGGAGACC	1680
DB	1621	AGACGACAGCCCTTACGCCACCCCTGCACTGGGGAGGAGAACATCACACGCTGGAGACC	1680
QY	1681	CCCTACCTGGAATTAACACACCTGAGGATCTCTCAATGATATACGTGGCGCTCTACTCC	1740
DB	1681	CCCTACCTGGAATTAACACACCTGAGGATCTCTCAATGATATACGTGGCGCTCTACTCC	1740
QY	1741	ATTGCTCAGCCCTTGAAGACATCCACTCTTGAACACCGGACCGGCACTTTTGCAAAAC	1800
DB	1741	ATTGCTCAGCCCTTGAAGACATCCACTCTTGAACACCGGACCGGCACTTTTGCAAAAC	1800
QY	1797	ATTGCTCAGCCCTTGAAGACATCCACTCTTGAACACCGGACCGGCACTTTTGCAAAAC	1797
DB	1797	ATTGCTCAGCCCTTGAAGACATCCACTCTTGAACACCGGACCGGCACTTTTGCAAAAC	1797
QY	1801	GGATCTTTGTCAGATATTAATAAAGTTGAGGCTTGGAGCTCTCAACCATCTGCTGCAT	1860
DB	1801	GGATCTTTGTCAGATATTAATAAAGTTGAGGCTTGGAGCTCTCAACCATCTGCTGCAT	1860
QY	1861	CTGAGTTTACCAACAGCATGGGTGAGGATTTGACTTTGACGATCAAGTGAACCTCAAG	1920
DB	1861	CTGAGTTTACCAACAGCATGGGTGAGGATTTGACTTTGACGATCAAGTGAACCTCAAG	1920
QY	1917	CTGAGTTTACCAACAGCATGGGTGAGGATTTGACTTTGACGATCAAGTGAACCTCAAG	1917
DB	1917	CTGAGTTTACCAACAGCATGGGTGAGGATTTGACTTTGACGATCAAGTGAACCTCAAG	1917
QY	1921	GGGAATCTACACCATTTAACTGGCAGCTCTCCGACAGAGGATGAATCGGTGTTGTTCCAT	1980
DB	1921	GGGAATCTACACCATTTAACTGGCAGCTCTCCGACAGAGGATGAATCGGTGTTGTTCCAT	1980
QY	1977	GGGAATCTACACCATTTAACTGGCAGCTCTCCGACAGAGGATGAATCGGTGTTGTTCCAT	1977
DB	1977	GGGAATCTACACCATTTAACTGGCAGCTCTCCGACAGAGGATGAATCGGTGTTGTTCCAT	1977
QY	1981	GAGGTGGGCAACTACAAACGCTACGTTAAGCCAGTGAACGAGTCAACATCAACGAAAG	2040
DB	1981	GAGGTGGGCAACTACAAACGCTACGTTAAGCCAGTGAACGAGTCAACATCAACGAAAG	2040
QY	2037	GAGGTGGGCAACTACAAACGCTACGTTAAGCCAGTGAACGAGTCAACATCAACGAAAG	2037
DB	2037	GAGGTGGGCAACTACAAACGCTACGTTAAGCCAGTGAACGAGTCAACATCAACGAAAG	2037



2041 AAAATCCTCTGAGTGGCTTCTCCAAAGTGGTTCCTTCTCCAACTGCGAGACTGT 2100  
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2101 GTCCGGGACACAGGAAGGGATCATCGAGGGGAGCCCACTGCTGCTTTTGAATGCATG 2160  
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2158 GCATGTGAGAGGAGAGTTAGTGAATGAACAGATGCAAGTGGTGTACAAAGTGGCCG 2217  
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2218 AATGATTTCTGTCGAATGAGAACACACGCTGCTGATCGCCAGAGAGATCGAGTACCTG 2277  
2281 TCGTGAAGAGAGCTTTCGGGATCGCTGACCATCTTTCGCGTACTCGGGCATCTGATC 2340  
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2341 ACCTCTTCTGCTGGGCTTTCATCAAGTTTCAGGAACACTCCCATCGTGAAGGCCACC 2400  
2338 ACCTCTTCTGCTGGGCTTTCATCAAGTTTCAGGAACACTCCCATCGTGAAGGCCACC 2397  
2401 AACCGGGAGTTGCTTACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCTTCAGCTCGCTC 2460  
2398 AACCGGGAGTTGCTTACCTGCTGCTCTTCTCCCTCATCTGCTGCTTCTTCAGCTCGCTC 2457  
2461 ATCTTCAATCGGAGCCGAGGACTGAGACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520  
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2521 AGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580  
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2641 CTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2700  
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2821 TGCTTCTTCTGCTTCAAGTCCCGTAAGCTGCGGAGAACTTCAACGAGGCTAAGTTC 2880  
2818 TGCTTCTTCTGCTTCAAGTCCCGTAAGCTGCGGAGAACTTCAACGAGGCTAAGTTC 2877  
2881 ATCACTTCCAGGATGATCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940  
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3001 GGGCTGCTGGGTGCAATTTACTTCAACAAAGTGTATCATCATCTGTTTCAAGCGTGGCT 3060  
2998 GGGCTGCTGGGTGCAATTTACTTCAACAAAGTGTATCATCATCTGTTTCAAGCGTGGCT 3057  
3061 AACACCATGAGAGTGGCTGCGACAGGGGGCCAGCGCTTCAAGTGGCGGCGCGG 3120  
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3298 ACAGGCGGATACGCCACCTCTAGCCGCGAGCGCGCGAGGAACTTCGGCGGATGCGCGC 3357  
3361 AGCGGCGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420  
3358 AGCGGCGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3417  
3421 CAGCGCGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3480  
3418 CAGCGCGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3477  
3481 GCGGCGAGAGGAGCG 3540  
3478 GCGGCGAGAGGAGCG 3537  
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3538 CCAAGAACTCTCTCCAGCGCAGCACGCTGCAACCTGACATCAACTCTTCAACCGTGGC 3597  
3601 TGCCCAACCTCTCCCTCTCCGCGCATTGCGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 3660  
3598 TGCCCAACCTCTCCCTCTCCGCGCATTGCGGTTTCTGCTGCTGCTGCTGCTGCTGCTGCT 3657  
3661 TCCTTTTATCCCTGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720  
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3718 ATATGAGTTGCAAAATAGGTGAGCAGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3777  
3781 ATCTGAACTACTTATTTCTCTCGAATGTAATCAAACTTGAAGTATTTTGTAGTACA 3840  
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3841 TTATGTTCTAACATTTGTAAGATAATTTGTTAACAATATAAGGTACCACTGAAAGCAGT 3900  
3838 TTATGTTCTAACATTTGTAAGATAATTTGTTAACAATATAAGGTACCACTGAAAGCAGT 3897  
3901 GACTGAGATTGCCACTGCTGATGAGCAGAACTGTTTATTAACATTTATCATTTGAAACCTGGA 3960  
3898 GACTGAGATTGCCACTGCTGATGAGCAGAACTGTTTATTAACATTTATCATTTGAAACCTGGA 3957  
3961 TTGCAACAGGAATATAATGACTGTAAACAAAATTTGTTGATTTCTTAAATGCAAAAT 4020  
3958 TTGCAACAGGAATATAATGACTGTAAACAAAATTTGTTGATTTCTTAAATGCAAAAT 4017  
4021 TGTAAATCAGATGTGTAATAATTTGTTGATTTCTTCTGTAATTTAAATGCAATTTCTTGATA 4080  
4018 TGTAAATCAGATGTGTAATAATTTGTTGATTTCTTCTGTAATTTAAATGCAATTTCTTGATA 4077  
4081 AAGCGCGCGCGCGCGCGCGCG 4134  
4078 AAGCGCGCGCGCGCGCGCGCG 4131

RESULT 8  
AAZ31049  
ID AAZ31049 standard; cDNA; 3234 BP.  
XX  
AC AAZ31049;

XX DT 07-JAN-2000 (first entry)  
 XX DE Human Car coding sequence.  
 XX KW G-protein fusion receptor; Car; calcium receptor; GluR; head injury;  
 XX KW metabotropic glutamate receptor; GABAR; chimeric receptor; stroke;  
 XX KW gamma-aminobutyric acid receptor; allosteric modulator; antagonist;  
 XX KW spinal cord injury; epilepsy; ischemia; hypoglycaemia; anoxia;  
 XX KW Alzheimer's disease; hyperparathyroidism; osteoporosis; depression;  
 XX KW cognitive disorder; ss.  
 XX OS Homo sapiens.  
 XX PN W09951641-A1.  
 XX PD 14-OCT-1999.  
 XX PF 02-APR-1999; 99MO-US007333.  
 XX PR 03-APR-1998; 98US-0080671P.  
 XX PA (NPSP-) NPS PHARM INC.  
 XX PI Stormann TM, Hammerland LG, Storjohann LL, Busby JG, Garrett JE,  
 XX PI Simin RT;  
 XX DR WPI; 1999-610995/52.  
 XX DR P-PSDB; AAY49105, AAY49110, AAY49115.  
 XX PT New G-protein fusion receptors and chimeras containing domains from  
 XX PT different receptors, used to screen for modulators, potentially useful  
 XX PT e.g. for treating or preventing stroke or Alzheimer's disease.  
 XX PS Disclosure; Fig 5; 255pp; English.  
 XX CC The invention relates to G-protein fusion receptors (I) comprising: (1)  
 XX CC in the N to C direction, extracellular (ECD), transmembrane (TMD) and  
 XX CC intracellular (ICD) domains, each chosen independently from a CAR  
 XX CC (calcium receptor), GluR (metabotropic glutamate receptor) and GABAR  
 XX CC (gamma-aminobutyric acid receptor); (2) an optional linker attached to  
 XX CC the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the  
 XX CC linker. (I), and recombinant chimeric receptors (CR) without the GP  
 XX CC component, are used to assess function of the various domains and to  
 XX CC identify compounds (e.g. allosteric modulators or antagonists) that act  
 XX CC on these domains. The modulators are potentially useful for treating or  
 XX CC preventing diseases associated with the receptors, e.g. stroke, head or  
 XX CC spinal cord injury, epilepsy, ischemia, hypoglycaemia, anoxia,  
 XX CC Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive  
 XX CC disorders and depression. Nucleic acid (II) that encodes (I) is used: (1)  
 XX CC for recombinant production of corresponding proteins; and (2) to produce  
 XX CC cells used in screening for modulators. Use of Car and mGluR domains  
 XX CC allows presentation of GABAR domains, to a binding agent, in a form more  
 XX CC like the natural domain structure compared with use of incomplete  
 XX CC receptors, lacking one or more domains. By shuffling different domains,  
 XX CC agents can be identified that affect particular domains of a receptor  
 XX SX Sequence 3234 BP; 739 A; 931 C; 829 G; 735 T; 0 U; 0 Other;  
 XX  
 Query Match 42.2%; Score 1745.2; DB 2; Length 3234;  
 Best Local Similarity 76.4%; Pred. No. 5.8e-300;  
 Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;  
 XX 501 CTCAGGGTATGTCCTCAAAACCAAGGCGCCAGAGAAAGAGACATCATCTGGAGGGTCT 560  
 DB 51 CTCCTGCTACGGGCGAGACACAGGAGCCCAAGAGAGGGGACATATCTCTGGGGGCT 110  
 XX 561 CTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGACTTTAAATCGAGACCGAGGC 620  
 DB 111 CTTTCCTATTCTTTGGAGTAGCAGCTAAAGATCAAGATCTCAATCAAGCCCGGAGTC 170  
 XX 621 GACAAATGATTCGGTACAAATTTTCGAGGCTTCGATGGCTCCAGGCGATGATTCGC 680

171 TGTGGAATGATCAGGTATAATTTCCGTGGGTTTGGCTGTACAGGCTATGATATTGC 230  
 581 AATTGAGAGATTAAACACAGATGACTTTCTCGCCCAATATCACCTGGGATCGCAT 740  
 231 CATAGAGAGATAAACAGAGCCCGAGCCCTTTCTCCCACTTACCGCTGGGATACAGAT 290  
 741 ATTTGACACCTGTAAACACCGTGTCCAAAGGCGCTAGAGGCAACACTCAGCTTTGTGCCCCA 800  
 291 ATTTGACACTTGCAACACCGTTTCTAAGGCTTGGAGCCACCTGAGTTTGTGTGCTCA 350  
 801 GAACAAATGACCTCGCTGAACTTAGATGAGTTCTGTAACTGCTCTGACCAATATCCATC 860  
 351 AACAAATATGATTTCTTTGAACCTTGATGAGTTCTGCACTGCTCAGAGACATTCCTC 410  
 861 CACAATAGCAGTGTGCGGGCAACCGGCTCAGGAATCTCCACGGCTGTGGCCCAATCTATT 920  
 411 TACGATTGCTGTGTGGAGCAACTGCTCAGGCTCTCCACGGCAGTGGCAATCTGCT 470  
 921 GGGATTAATTTTACATTCACAGGTGAGTATGCTCTCTGAGCAGGCTGCTCAGCAACAA 980  
 471 GGGCTCTTCTTACATTCCTCCAGGTGAGTTATGCTCTCTCAGCAGACTCTCTCAGCAACA 530  
 981 GAATGAGTACAAAGCCCTTCTGAGGACCATCCCAATGATGAGCAACAGAGCCACGCCAT 1040  
 531 GAATCAATTCAGTCTTTCTTCGACCCTCCCAATGATGAGCAACAGAGCCACTGCTAT 590  
 1041 GGCAGGATCATCGAGCACTTCCAGTGGAACTGGGTGGGAACTCCGCGCCAGCAATGA 1100  
 591 GGCAGACATCATCGAGTATTTCCGCTGGAATCGGTGGGCAAAATTCGAGCTGATGACGA 650  
 1101 CTATGGCCGCCAGGCAATTCAGAGTTCCGGAGGAGGCGCTTAAGAGGACATCTGAT 1160  
 651 CTATGGCCGCCCGGGGATTGAGAAATTCGAGAGGAGCTGAGGAAAGGATATCTGCAT 710  
 1161 TGACTTCAGTGCAGATGATCTCTCAGTACTACACCCAGAGAGCTTGGAGTTTCATCCCGCA 1220  
 711 CGACTTCAGTGAATCACTCTCCAGTACTCTGATGAGGAAGAGATCCAGCATGTGTAGA 770  
 1221 GTCATCCAGAACTCTCGGCCAAGGTATCTGCTGCTTCTCCAAATGGCCCGACCTGA 1280  
 771 GGTGATTCAAAATTCACCGCCAAAGTATCTGCTGCTTCTCCAGTGGCCCGACATCTGA 830  
 1281 GCGCTCATCCAGAGATAGTTCGGAGAAACATCACCGATCGGATCTGCTGGCCAGCGCA 1340  
 831 GCGCTCATCCAGAGATAGTTCGGAGAAATTCGGGCGCATATACGGGCAAGATCTGCTGGCCAGCGCA 890  
 1341 GCGTGGCCAGCTCTTCTGCTCATATTCGCAAGCAGAGTACTTCCAGTGGTGGCGGAC 1400  
 891 GCGCTGGCCAGCTCTCTCTCCCTGATCGCCATGCTCAGTACTTCCAGTGGTGGCGGAC 950  
 1401 CATCGCTTCGCTCTCAGGCGGGGTATCCAGAGGTTCAACAAGTCTCTGAAGAGGT 1460  
 951 CATGGATTGCTCTGAAGGCTGGGAGATCCAGGCTTCCGGGAATTCCTGAAGAGGT 1010  
 1461 CCACCCAGCAGGTCTCTCGACAAATGGGTTTGTCAAGAGGTTCTGGAGAGACCTTCAA 1520  
 1011 CCATCCAGGAGTCTGTCCACAATGGTTTGGCAAGGAGTTTGGGAAGAAACATTTAA 1070  
 1521 CTGCTACTTCCAGAGAGACCTCTGAGCGAGCTGAAGAATTCGAAGTGGCTTCGCGACCG 1580  
 1071 CTGCCACCTCAAAGA-----AGTGTCAAAGGAGACCTTTACTCTGGACACTTTCTG 1122  
 1581 ACCGGCGCTCAAGGGGACGGCTCCAAAGCGGGGAACTCCAGAGCAGACAGCCCTACGCCA 1640  
 1123 AGAGG----TCAGAGAGAGTGGCGCAGAGTTTAGCAACAGCTCGACAGCTTCGACC 1178  
 1641 CCCTGTCATGGGGAGAGAAATCATACCGGTGGAGAGCCCTCTACTCTGATTTATACAA 1700  
 1179 CCTCTGTACAGGGGATGAGAAATCAGCAGTGTGCGAGAGCCCTTTACATAGATTACACGA 1238  
 1701 CCTGAGGATCTCTACAATGTATACGTGGCGGCTACTCCATTGCTCAGCCCTGCAAGA 1760  
 1239 TTTACGAGATCTCTACATGTGTACTTAGCAGTCTACTCCATTGCCAGCCCTTGAAGA 1298

QY 1761 CATCACTCTTTGAAACCCGACGGGCATCTTTGCAACCGATCTTTGTGAGATATTA 1820  
Db 1299 TATATATACCTTGTACCTTGGAGAGGCTCTTCAACGATGGCTCTGTGAGACATCAA 1358  
QY 1821 AAAAGTTGAGGCTGGAGGCTCTCAACATCTGTGTGATCTGAAGTTTACCAACAGCAT 1880  
Db 1359 GAAAGTTGAGGCTGGAGGCTCTGAAGACCTACGGCATCTAAACCTTTTACAAACAATAT 1418  
QY 1881 GGGTGAGCAGGTTGACTTTTGAAGATCAAGGTGACCTCAAGGGGAACATACACATTAATCAA 1940  
Db 1419 GGGGAGCAGGTTGACCTTTTGAAGATGAGTGTGATGCTGTGGGGAACATATTCATCATCAA 1478  
QY 1941 CTGCAGCTCTCCGAGAGGATGAATCGGTGTGTTCATCAAGGTGGGCAACTACAACGC 2000  
Db 1479 CTGCAGCTCTCCGAGAGGATGGCTCCATCGTGTAAAGGAAGTCGGGTATTAACAAGT 1538  
QY 2001 CTACCTTAAGCCAGTGAACGACCTCAACATCAAGGGAAGAAATCTCTCGAGTGGCTT 2060  
Db 1539 CTATGCCAAGAGGAGAAAGACTCTTCAACAGGAGAAATCTCTGTGGAGTGGGT 1598  
QY 2061 TCCCAAGTGGTCTCTCAACTGAGTGCAGTGTGTGCGGGSCACACGGAAGGG 2120  
Db 1599 TCCAGGAGGTCCTTCTCAACTGAGCGGACTGCTGGCAGGACACGGAAGG 1658  
QY 2121 GATCATCGAGGGGAGCCCACTGTCTTGAATGATGGAATGTCAGAGGAGAGT 2180  
Db 1659 GATCATCGAGGGGAGCCCACTGTCTTGAATGATGGAATGTCAGAGGAGT 1718  
QY 2181 CAGTCATGAACAGTGAAGTGCCTGACAAAGTCCCGAATGATTTCTGTGCAATGA 2240  
Db 1719 TAGTGAATGACAGATGTCAGTGCCTGTAACAGTCCCGAATGATTTCTGTGCAATGA 1778  
QY 2241 GAACACACGTCGTGCATCGCAAGAGATCGAGTACCTGTGTGGAGCGGAGCCCTGG 2300  
Db 1779 GAACACACCTCTGCTTGCAGAGATCGAGTTCCTGTGTGGAGCGGAGCCCTTGG 1838  
QY 2301 GATCGCTGACCATCTTCCGCTACTGGGATCTGATCACTCTTCTGTGTGGGCT 2360  
Db 1839 GATCGCATCACCTCTTTCGCTGCTGGGATTTCTCTGACAGCTTTGTGTGGGCT 1898  
QY 2361 CTTCATCAAGTTTCAGGAACACTCCCATCGTGAAGGCCACCAACCGGGAGTTGTCTACCT 2420  
Db 1899 GTTTATCAAGTTCCGACACACACACCATTTGTAAGGCCACCAACCGAGAGCTCTCTACCT 1958  
QY 2421 GTGCTCTTCTCCTCATCTGCTTCTCAGCTCGCTCATCTTTCATCGGGAGCCAG 2480  
Db 1959 CCTCCTCTTCTCCTGCTGCTGCTTCTCAGCTCCTGTCTTTCATCGGGAGCCCA 2018  
QY 2481 GGAAGTGGACCTGTGGCTCGGCAACCGGCTTTGGCATCAGTTCGTCCTGTGATCTC 2540  
Db 2019 GGAAGTGGACCTGTGGCTCGGCAACCGGCTTTGGCATCAGTTCGTCCTGTGATCTC 2078  
QY 2541 CTGCATCTGTGTAAGAACCAACCGGCTGTGTGTCTGAGGCAAGATCCCCACAG 2600  
Db 2079 ATGCACTCTGTGTGAAACCAACCGGCTGTGTGTGAGGCAAGATCCCCACAG 2138  
QY 2601 CTTCACCGGAGTGGTGGGCTCAACCTGAGTTCCTCTGCTTCTCTGATCCT 2660  
Db 2139 CTTCACCGGAGTGGTGGGCTCAACCTGAGTTCCTCTGCTTCTCTGATCCT 2198  
QY 2661 GGTGCAAAATCGTCACTGATCATCTGGCTCTACACCGGCTCCTCTCAGTACAGGAA 2720  
Db 2199 CATGCAAGTTGATCTGTGTGATCTGGCTCTACACCGGCTCCTCTCAGTACAGGAA 2258  
QY 2721 CATGAGCTGGAGGAGGATCATCTTCACTACCTGCGAGGAGGCTGCTCATGGGCT 2780  
Db 2259 CCAGGAGCTGGAGGATGATCATCTTCACTGCTGCGAGGAGGCTCCTCATGGGCT 2318  
QY 2781 GGGCTTCTCATCGGCTACACCTGCTCCTGCGGCAATCTCTTCTTCTGCTGCTCAA 2840  
Db 2319 GGGCTTCTCATCGGCTACACCTGCTCCTGCTGCTGCTGCTGCTGCTGCTGCTCAA 2378

QY 2841 GTCCCTTAAGCTGCCGAGAACTTCAACGAGGTAAGTTTCATCACCTTCAGCATGTTGAT 2900  
Db 2379 GTCCCGAAGCTGCCGAGAACTTCAATGAAGCAAGTTTCATCACCTTCAGCATGTTGAT 2438  
QY 2901 CTTCTTCACTGCTGTGATCTCTTCAATCCCGCTATGTCAGCACCTACGGCAAGTTGT 2960  
Db 2439 CTTCTTCACTGCTGTGATCTCTTCAATCCCGCTATGTCAGCACCTACGGCAAGTTGT 2498  
QY 2961 GTCCGCGTGGAGTGATTCCTCATCTGCTTCAAGGTCGAGCTTGGCTTGGCTGCTGCT 3020  
Db 2499 CTCTGCGTAGAGGTGATTCCTCATCTGCTTCAAGGTCGAGCTTGGCTTGGCTGCTGCT 2558  
QY 3021 CTTCAACAGTGTATCATCATCTGCTTCAAGGTCGAGCTTGGCTTGGCTGCTGCTGCT 3080  
Db 2559 CTTCAACAGTGTATCATCATCTGCTTCAAGGTCGAGCTTGGCTTGGCTGCTGCTGCT 2618  
QY 3081 CTGAGCACCGCGGCTGAGCTTCAAGGTCGAGCTTGGCTTGGCTGCTGCTGCTGCTGCT 3140  
Db 2619 TTGAGCACCGCGGCTGAGCTTCAAGGTCGAGCTTGGCTTGGCTGCTGCTGCTGCTGCT 2678  
QY 3141 CGGCTTCTGCAAGCTTCAAGGTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 3200  
Db 2679 CGTCTCCGCAAGCTTCAAGGTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 2738  
QY 3201 CACTCGGCGGCTGAGCTTCAAGGTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 3260  
Db 2739 CATGAGCACGAGCAACA-----CGAGAGCTTCCACAGCCCGAGAGGAGAG 2793  
QY 3261 CGGAGCGGCAAGCTTCAAGGTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 3320  
Db 2794 CAGCAGCGGCTGAGCTTCAAGGTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 2853  
QY 3321 CAGCAGCGGCTGAGCTTCAAGGTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 3362  
Db 2854 CAGCAGCAAGCTTCAAGGTCGAGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 2895

RESULT 9  
AA90922  
ID AAX90922 standard; DNA; 3234 BP.  
XX  
AC AAX90922;  
XX  
DT 17-JAN-2000 (first entry)  
XX  
DE Human calcium receptor nucleic acid sequence.  
XX  
KW Human calcium receptor; GABABR modulator; GABABR receptor protein;  
KW gamma-aminobutyric acid receptor; metabotropic receptor;  
KW chimeric protein; synaptic transmission; extracellular binding domain;  
KW antagonist activity; intracellular domain; intracellular effect; ds.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3234  
FT /\*tag= a  
FT /product= "Human calcium receptor protein"  
XX  
PN WO9951636-A2.  
XX  
PD 14-OCT-1999.  
XX  
PF 02-APR-1999; 99WO-US007352.  
XX  
PR 03-APR-1998; 98US-0080676P.  
XX  
PA (NPS-) NPS PHARM INC.  
XX  
PI Garrett JE, Simin RT, Busby JG, Stormann TW;  
XX WPI; 1999-610994/52.  
XX P-PDB; AAY28840.  
DB

XX Novel nucleic acids, used to screen for specific modulators, e.g. for  
 PT treating spasticity or Alzheimer's disease.  
 XX Disclosure; Fig 3A-3D; 78pp; English.  
 XX The present sequence is the human calcium receptor nucleic acid sequence.  
 CC This is used in assaying for compounds modulating GABAR activity. GABAR  
 CC receptors are metabotropic receptors that modulate synaptic transmission  
 CC in brain. Portions of calcium receptor are swapped with portions of  
 CC GABAR2 to create protein fusions. The agonist extracellular binding  
 CC domain is swapped for measurement of antagonist activity. Intracellular  
 CC domains are swapped for measuring intracellular effects caused by the  
 CC different receptor  
 XX Sequence 3234 BP; 739 A; 931 C; 829 G; 735 T; 0 U; 0 Other;

Query Match 42.2%; Score 1745.2; DB 2; Length 3234;  
 Best Local Similarity 76.4%; Pred. No. 5.8e-300;  
 Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;

QY 501 CTCAGGGTATGGTCCAAACCAAGGCCCCAGAGAAAGGAGACATCATACTGGGAGGTCT 560  
 DB 51 CTCGCTACGGGCCAGACAGCGAGCCCAAGAGAGGGGACATTTATCTTTGGGGGCT 110  
 QY 561 CTTCCTCAATACACTTTGGAGTAGCCGCCAAGGATCAGGACTTAAATCGAGACCGGAGC 620  
 DB 111 CTTTCCTATTCATTTTGGAGTAGCAGCTAAAGATCAAGATCTCAATCAAGGCCGGAGTC 170  
 QY 621 GACAAATGTATTCGGGTACAAATTTTCGAGGCTTCGAGTTCGAGGCGATGATATTCGC 680  
 DB 171 TGTGGAAATGATCAGGTATTAATTCGTGGTTCGCTGGTTACAGGCTATGATATTTGC 230  
 QY 681 AATTGAAGAGATTAAACAGTATGACTTTCCTGCCAATATCACCTCGGAGATTCGGAT 740  
 DB 231 CATAGAGGAGATAAACAGCAGCCAGCCCTTCTCCCACTTTGAGCCTGGGATACAGGAT 290  
 QY 741 ATTGACACGTGTAAACACCGTGTCCAAAGCGCTAGAGGCAACACTCAGCTTTGTGGCCCA 800  
 DB 291 AATTGACACTTGAACACCGCTTCTAAGGCCCTTGAAGCCACCTGAGTTTGTGTCTCA 350  
 QY 801 GAACAAATCGACTCGCTGAACTTAGATGAGTCTGTAACTGCTCTGACCAATATCCCATC 860  
 DB 351 AAACAAATTTGATTTCTTTGAACTTGTGAGTCTCTGCAACTGCTCAGAGCACTATCCCTC 410  
 QY 861 CACATAGCAGTGGTGGGGCAACCGGTCAGGATCTCCAGGCTGTGGCCATCTATT 920  
 DB 411 TAGGATGTGTGGTGGGAGCAACTGGCTCAGGCGTCTCCAGCGAGTGGCAATCTGCT 470  
 QY 921 GGGATTTATTTTACATTCACAGGTGAGCTATGCTCTCTCGAGCAGGCTGCTCAGCAACA 980  
 DB 471 GGGGCTCTTCTACATTTCCCGAGTCACTGATGCTCTCTCCAGCAGACTCTCAGCAACA 530  
 QY 981 GAATGATACAGGCTCTCTGAGACCAATCCCAATGATGAGCAACAGGCAACGGCCAT 1040  
 DB 531 GAATCAATTTCAAGTCTTTCTCCGACCACTCCCAATGATGAGCAACAGGCACTGCGCAT 590  
 QY 1041 GGCAGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGAACCTTGGCAGCGCAGATGA 1100  
 DB 591 GGCAGACATCATCGAGTATTTCCGCTGGNACTGGGTGGGCACAAATTTGACGCTGATGAGA 650  
 QY 1101 CTATGGCCGCCAGGCAATGAACAAGTTCGGAGAGGCGGTTAAGAGGCACTCTGAT 1160  
 DB 651 CTATGGCGCGCGGGGATTTGAGAAATTCGAGAGGAAGCTGAGGAAGGGATATCTGCAT 710  
 QY 1161 TGACTTTCACTGAGATGATCTCTCAGTACTTACACCAGAGCAGTTTGGAGTTTCATGCCGA 1220  
 DB 711 CGACTTTCAGTGAATCTATCTCCAGTACTCTGATGAGGAAGATCCAGCATGTGTTAGA 770  
 QY 1221 CGTATCCAGAACTCTCTCGGCCAAGGTATCATGTGTCTTCTCCAAATGCCCGGACCTGGA 1280  
 DB 771 GGTGATTCAAATTTCCACGGCCAAAGTCACTGTGGTTTCTCCAGTGGGCCAGATCTTGA 830

QY 1281 GCCCTCATCCAGGAGATAGTTCCGAGAAACATCACGATCGATCTGGCTGGCCACGCA 1340  
 DB 831 GCCCTCATCAAGGAGATTCGCGGGCAATATCACGGCAAGATCTGGCTGGCCACGCA 890  
 QY 1341 GGCTTGGCCAGCTCTTCGCTCATTCGCAAGCCAGAGTACTTCCAGCTGTGCTGGCCGAC 1400  
 DB 891 GGCTTGGCCAGCTCTTCGCTCATTCGCAAGCCAGAGTACTTCCAGCTGTGCTGGCCGAC 950  
 QY 1401 CATCGGCTTCGCTCTCAGGGCGGGGCTATCCAGAGGTTCAACAAGTCTCTGAAGAGGT 1460  
 DB 951 CATTTGATTCGCTCTGAAGCTCGGCAGATCCAGAGGCTTCGGGAATTCCTGAAGAAGT 1010  
 QY 1461 CCACCCAGCAGGTCCTCGGACAAATGGTTTGTCAAGGAGTCTGGGAGGAGACCTTCAA 1520  
 DB 1011 CCATCCCAAGGAGTCTGTCCCAATGGTTTTCGAAGGAGTTTGGGAAGAAACATTTAA 1070  
 QY 1521 CTGCTACTTCACCGAGAAGACCTCGACGAGCTGAAGAATTCGAAGGTGCCCTCGCACGG 1580  
 DB 1071 CTGCCACTCCAGA-----AGTGTCAAAGGACCTTTACTGTGGACACTTTCTG 1122  
 QY 1581 ACCGCGGCTCAAGGGGACGGCTCCAAAGCGGGGAACTCCAGACGGACAGCCCTACGCCA 1640  
 DB 1123 AGAGG-----TCAGCAAGAAAGTGGCGACAGGTTTAGCAACAGCTCGACAGCTTCGAGC 1178  
 QY 1641 CCCTGCACTGGGAGGAGAACATCACACGCTGGAGACCCCTACTCTGATTTATACACA 1700  
 DB 1179 CCTCTGTACAGGGGATGAGAAATCAGCAGTGTGAGAACCCCTTACATAGATTACAGCA 1238  
 QY 1701 CCTGAGGATCTCTCAATGTATATACGTGGCGCTACTCTCAATGTCTCAGCCCTCGAAGA 1760  
 DB 1239 TTTAGGATATCTCAATGTATCTAGCAGTCTACTCAATGCCACGCTTCGCAAGA 1298  
 QY 1761 CATCCACTCTTCAAAACCCGGACGGGCTCTTTGCAAGGATCTGTGCGAGATTTAA 1820  
 DB 1299 TATATATACCTGTCTACCTGGGAGAGGCTCTTCAACCAATGGCTCTGTGCGAGACATCA 1358  
 QY 1821 AAAAGTTGAGGCTTCGAGGCTCTCAACCATCTGCTGCACTCTGAAGTTTACCAACAGCAT 1880  
 DB 1359 GAAAGTTGAGGCTTCGAGGCTCTCAAGCAGCTTACGCACTCTAAACTTTTACAAACAAT 1418  
 QY 1881 GGTGAGCAGGTTGACTTTGACGATCAAGTGAACCTCAAGGGAACTACACCATTTATCAA 1940  
 DB 1419 GGGGAGCAGGTCACCTTTGATGAGTGTGGTGACCTTGGTGGGAACTATTTCCATCATCAA 1478  
 QY 1941 CTGGCAGCTCTCCGAGAGGATGAATCGGTGTGTTCATGAGTGGGCAACTTACAACGC 2000  
 DB 1479 CTGGCAGCTCTCCGAGAGGATGGCTCCATCGTGTTTAAGGAAGTCGGGTATTACAACT 1538  
 QY 2001 CTAGCTTAAGCCCAAGTGAACGACTCAACATCAACGAAAGAAATCTCTGAGTGGCTT 2060  
 DB 1539 CTATGCCAAGAGGAGAAAGACTCTTTCATCAACGAGGAGAAATCTCTGAGTGGGT 1598  
 QY 2061 CTCCAAAGTGGTTCCTTTCTCCAACTGCACTGAGACTGTGCGGGCAGCAGGAGAGG 2120  
 DB 1599 CTCAGGAGGTCCTTCTTCCAACTGCAAGCAGGACTGCTGGCAGGAGCAGGAAAGG 1658  
 QY 2121 GATCATCGAGGGGAGCCCACTCTGCTTGAATGCAATGGCATGTGCGAGAGGAGATT 2180  
 DB 1659 GATCATTTAGGGGGAGCCCACTCTGCTTGAATGCTGTGGAGTGTCTGTATGGGAGTA 1718  
 QY 2181 CAGTGTAGAAACGATGCAAGTGTGCAAGTGTCCCGAATGATTTCTGTGTCGATGA 2240  
 DB 1719 TAGTGTAGACAGATGCCAGTGTCTTAACTGCAAGTGTCCAGATGACTTTCTGTGCCAATGA 1778  
 QY 2241 GAACCAACCTCTGTGATCGCCAAAGGAGATCGAGTACCTGTCTGTGACGAGGAGCTTCGG 2300  
 DB 1779 GAACCAACCTCTGTGATTTGCCAAGGAGATCGAGTGTCTGTGACGAGGAGCTTTGG 1838  
 QY 2301 GATCGCTGTGACCATCTTTCGCGGTACTGGGGCATCTGTGATCACTCTTCTGTGCTGGGGGT 2360  
 DB 1839 GATCGCACTCACCTCTTTCGCGGTGTGGGCAATTTTCTGTGACAGGCTTTGTCTGGGTGT 1898  
 QY 2361 CTTTCATCAAGTTTCAAGAAACACTTCCCATCGTGAAGGCCCAACCCGAGGTTGTCTTACCT 2420





Db 411 TAGGATTGCTGTGGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAATCTGCT 470  
Qy 921 GGGATTATTTTACATTCCACAGGTAGCTATGCTCTCTCGAGAGGCTGCTCAGCAACA 980  
Db 471 GGGGCTCTTCTACATTCCCAAGGTCACTATGCTCTCTCCAGCAGACTCTCAGCAACA 530  
Qy 981 GAATGAGTACAGGCTCTCTGAGAGCACTCCCAATGATGAGCAACAGGACCGGCAT 1040  
Db 531 GAATCAATTTCAAGTCTTTCTCCGAAACCATCCCAATGATGAGCAACAGGACCGGCAT 590  
Qy 1041 GGGCAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGAAACCTCGGAGCGCAGATGA 1100  
Db 591 GGCAGACATCATCGAGTATTTCCGCTGGAATCTGGGTGGGCACAATTCAGCTGATGACGA 650  
Qy 1101 CTATGGCCGCCAGGCAATGACAAGTTTCGGGAGAGGCGGTTAAGAGGACATCTGTAT 1160  
Db 651 CTATGGCGCGCGGGGATTTGAGAAATTCGAGAGGAAGCTGAGGAAGGGATATCTGCAT 710  
Qy 1161 TGACTTTCAGTGAGATGATCTCTCAGTACTACACCCAGAGAGTTGGAGTTTCATCGCGCA 1220  
Db 711 CGACTTTCAGTGAATCACTCTCCAGTACTCTGATGAGGAAGATCCAGAGATGTTGATGA 770  
Qy 1221 CGTATCCAGAACTCTCTGGCCCAAGTCAATGCTGCTCTTCCAAATGSCCGGACCTGGA 1280  
Db 771 GGTGATTTCAAAATTCACCGCCAAAGTCACTGCTGCTTTTCTCCAGTGGCCGAGATCTTGA 830  
Qy 1281 GCGGCTCATCCAGGAGATGATTCGAGAGAAATCAACCGATCGGATCTGGCTGGCCAGCA 1340  
Db 831 GCGGCTCATCAAGGAGATGTCGCGGCAATATACGGGCAAGATCTGGCTGGCCAGGCA 890  
Qy 1341 GGCCTTGGGCGAGCTCTCTGCTCAATTCGCAAGCAGAGTACTTCCAGTGGTGGCGGCAC 1400  
Db 891 GGCCTGGGCGAGCTCTCTGCTGATCGCCATGCTCAGTACTTTCAGAGTGGTGGCGGCAC 950  
Qy 1401 CATCGGCTTCGCTCTCAGGGCGGGGATTCAGGAGTTTCAACAGTTCTGAGAGGAT 1460  
Db 951 CATTTGGATTCGCTCTGAAGGCTGGGAGATCCAGGCTTCGGGAAATTCCTGAGAGAGT 1010  
Qy 1461 CCACCCAGCAGCTCTCGCAATTTGGGTTTGTCAAAGAGTTCTGGGAGGAGACTTCAA 1520  
Db 1011 CCATCCAGGAGTCTGTCCCAATTTGGTTTGTCCAAAGAGTTTGGGAAGAAACATTAA 1070  
Qy 1521 CTGCTACTTCAACGAGAACCTCTGACGAGCTGAAGAAATTCGAAGTGGCTTCGCACGG 1580  
Db 1071 CTGCGACCTTCCAGG-----AGGTGCAAGAGACCTTTACCTGTGGACACCTTTCTG 1122  
Qy 1581 ACCGGGGCTCAAGGGAGCGGCTCAAGCGGGGAACTCCAGAGCAGAGCCCTACGCA 1640  
Db 1123 AGAGG-----TCAGGAAGAAAGTGGCGACAGGTTTACGAAACAGCTCCAGAGCTTCCGAC 1178  
Qy 1641 CCCCTGCACTGGGAGGAGAAATCAACAGGCTGGAGACCCCTACCTGGATTATACACA 1700  
Db 1179 CCTCTGTACAGGGATGAGAAATCAGCAGTGTGAGACCCCTTACATAGATTACACGCA 1238  
Qy 1701 CCTGAGGATCTCCTACAAATGATAGTGGCGCTACTCCTGCTGCTACGCGCTGCAAGA 1760  
Db 1239 TTTACGGATATCCTACAAATGATAGTGGCGCTACTCCTGCTGCTGCTGCTGCAAGA 1298  
Qy 1761 CATCCACTCTTGCAAAACCGGACCGGATCTTTGCAAAACGGATCTTGTGAGATATTAA 1820  
Db 1299 TATATATACCTTACCTGGGAGAGGCTCTTACCAATAGCTCTGCTGAGAGATCAA 1358  
Qy 1821 AAAAGTTGAGGCTGGCAGGCTCTCAACATCTGCTGATCTGAAGTTTACCAAGCAT 1880  
Db 1359 GAAAGTTGAGGCTGGCAGGCTCTGAAGCAGCTACGGCATCTAAATTTTACAAACAAT 1418  
Qy 1881 GGGTCAAGCAGGTTGACTTTGAGCACTCAAGGTGACCTCAAGGGGAACTACCAATATCAA 1940  
Db 1419 GGGGGGAGGCTGACCTTTGATGAGTGGTGGTGGCTGCTGCTGCTGCTGCTGCTGCTG 1478  
Qy 1941 CTGGCAGCTCTCCGAGAGGATGAATCGGCTGTTTCCATGAGTGGGCAACTCAACGC 2000  
Db 1479 CTGGCAGCTCTCCGAGAGGATGGCTCCATCTGTTTAAAGGAAGTCCGGTATTACAGCT 1538

Qy 2001 CTACGGTAAAGCCAGTGAACGACTCAACATCAACGAAAGAAATCTCTCTGAGTGGCTT 2060  
Db 1539 CTATGCAAGAGGGAGAGAAAGACTCTTTCATCAACGAGGAGAAATCTCTGAGTGGGTT 1598  
Qy 2061 CTCAAAGTGGTTCCTTTCTCCTCAACTGCACTGAGACTGTGCGCGGACACGAGAAAGG 2120  
Db 1599 CTCAGGGAGGTCCCTTTCTCCTCAACTGCACTGAGACTGCTGCGGAGGACACGAGAAAG 1658  
Qy 2121 GATCATCGAGGGGAGGCCCACTGCTGCTTTGAATGATGAGCATGTCAGAGGAGGAGTT 2180  
Db 1659 GATCAATGAGGGGAGGCCCACTGCTGCTTTGAGTGTGAGAGTGTCTGATGGGAGTA 1718  
Qy 2181 CACTGATGAAACGATGCAAGTGCCTGTAAGTGCCTGAAATGATTTCTGTCGAATCA 2240  
Db 1719 TAGTGATGAGACAGATGCGCAGTGCCTGTAACAAAGTGCCTGAGATGACTTCTGTCANTGA 1778  
Qy 2241 GAAACCAAGTCTGTCATCGCCAGGAGATCGAGTACTGTCGTGGACGAGGCCCTTGG 2300  
Db 1779 GAAACCAAGTCTGTCATTTGCGGATGCGAAGAGATCGAGTTCTGTCGTGACGAGCCCTTGG 1838  
Qy 2301 GATCGCTGACCATCTTTCGCGTACTGGGATCTGATCACTCTCTCTGCTGGGCT 2360  
Db 1839 GATCGCACTCACCTCTTTCGCGTGTGGGATTTTCTGACAGCTTTGTGCTGGGT 1898  
Qy 2361 CTTTCATCAAGTTTCAGGAACACTCCCATCGTGAAGGCCAACCAACCGGAGTTTCTCTACT 2420  
Db 1899 GTTTATCAAGTTTCGCAACACACACCATTTCAAGGCCAACCAACGAGAGCTCTCTACT 1958  
Qy 2421 GCTGCTCTTCTGCTCATCTGCTGCTTCTCAGTCTGCTCATCTTCATCGGAGAGCCAG 2480  
Db 1959 CTTCTCTCTCTGCTGCTGCTGCTTCTCAGTCTGCTTCTTCTCATCGGAGAGCCCA 2018  
Qy 2481 GGAAGTCAAGTTCGCTGCTGCTGCTGCTTGGCATCAGTCTGCTGCTGCTGCTGCTGCT 2540  
Db 2019 GGAAGTCAAGTTCGCTGCTGCTGCTGCTGCTTGGCATCAGTCTGCTGCTGCTGCTGCT 2078  
Qy 2541 CTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2600  
Db 2079 ATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2138  
Qy 2601 CTTCTCAACGAGTGGTGGGCTCAACCTGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCT 2660  
Db 2139 CTTCTCAACGAGTGGTGGGCTCAACCTGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCT 2198  
Qy 2661 GGTGCAAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2720  
Db 2199 CATGCAAGTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2258  
Qy 2721 CCATGAGTGGAGGAGAGTCTCTTTCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2780  
Db 2259 CCAGGAGTGGAGGAGTCTCTTTCATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2318  
Qy 2781 GGGCTTCTCTCATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2840  
Db 2319 GGGCTTCTCTCATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2378  
Qy 2841 GTCCGCTGAGTGGCGGAGACTTCAACGAGGTAAGTTTCATCACTGCTGCTGCTGCTGCTGCTGCT 2900  
Db 2379 GTCCGGAAGTGGCGGAGACTTCAATGAAGCAAGTTTCATCACTGCTGCTGCTGCTGCTGCTGCT 2438  
Qy 2901 CTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2960  
Db 2439 CTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2498  
Qy 2961 GTCCGCTGAGGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3020  
Db 2499 CTTCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2558  
Qy 3021 CTTTCACAAAGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3080  
Db 2559 CTTTCACAAAGTGTGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2618

OS	Homo sapiens.
XX	
PN	WC2004040000-A2.
XX	
PD	13-MAY-2004.
XX	
XX	09-SEP-2003; 2003WO-US028226.
XX	
XX	09-SEP-2002; 2002US-0409303P.
PR	09-APR-2003; 2003US-0461329P.
XX	
XX	(PRIM-) PRIMAL INC.
PA	
XX	
XX	Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI	Madisen L, McIlwain KU, Pavlova MN, Vassilatis D, Zeng H;
XX	
XX	WPI; 2004-390329/36.
DR	P-PSDB; ADO29211.
XX	
XX	Novel mammalian G protein coupled receptors, useful for identifying
PT	compounds that modulates diagnosing and treating disease condition
PT	associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT	pectoris, Parkinson's disease.
XX	
XX	Claim 151; SEQ ID NO 926; 542pp; English.
PS	
XX	

Seq	Sequence	3237 BP;	741 A;	931 C;	829 G;	736 T;	0 U;	0 Other;
Query Match	42.2%;	Score	1745.2;	DB	12;	Length	3237;	
Best Local Similarity	76.4%;	Pred. No.	5.9e-300;					
Matches 2187;	Conservative	0;	Mismatches	658;	Indels	17;	Gaps	3;
QY	501	CTCAGGGTATGGTCCAAACCAAGAGGCCCCAGAAAGGAGACATCATATCTGGAGGTCT	560					
DB	51	CTCTGCTCTAGGCGCCAGACCCAGCGAGCCCAAAAGAGGGGGACATTATCTCTGGGGGGCT	110					
QY	561	CTTCCCAAATACACTTTGGGAGTAGCCGCCAAGGATCAGGACTTAAAAATCGAGACCGGAGGC	620					
DB	111	CTTTCTATTTCATTTTGGAGTAGCAGCTAAGATCAAGATCTCAATCAAGGCCGGAGTC	170					
QY	621	GACAAAATGATTCGGTACAAATTTTCAGGCTTCCGATGGCTCCAGCGGATGATATTTCCG	680					
DB	171	TGTGGAATGTATCAGGTATAATTTCCGTGGTTTCGCTGGTTACAGGCTATGATATTTCG	230					
QY	681	AATTGAAGAGATTAAACAAAGTATGACTTTCGTGCCCAATATACACCTGGGATATCCGAT	740					
DB	231	CATAGAGGAGATAAACAGCAGCCAGCCCTTCTTCCCAACTTCAGCGTGGGATACAGGAT	290					
QY	741	ATTGTACAGCTGTAAACACCGTGTCCAAGGCGCTAGAGGGCAACACTCAGCTTTTGTGGCCCA	800					
DB	291	ATTGTACATTGCAACACCGTTTCTAAGGCTTTGGAAGCCACCCTGAGTTTTGTGTGCTCA	350					
QY	801	GAACAAAATCGACTCCCTGAACTTAGATGAGTTCTGTAACTGTCTGTACCAATATCCCATC	860					
DB	351	AAACAAAATTGATTCTTTGAAACCTTGATGAGTTCTGCAACTGTCTCAGAGCACATTCCTC	410					
QY	861	CACAAATAGCAGTGGTCGGGGCAACCGGTCAGGAATCTCCACGGCTGTGCCCAATCTATT	920					
DB	411	TAGGATTTGCTGTGGTGGGAGCAACTGGCTCAGCGGCTCTCCACGGCAGTGGCAAACTGCT	470					
QY	921	GGGATTATTTTTACATTTCCACAGGTTCAGCTATGCTCTCTCCAGCAGGCTGTCTCAGCAACAA	980					
DB	471	GGGGCTCTTCTACATTTCCCGCAGTTCAGTTATGCTCTCTCCAGCAGACTCTCTCAGCAACAA	530					
QY	981	GAATGAGTCAAGGCCCTTCTTGAGGACCATCCGCCAATGATAGGCAACAGGCCACGGGCAT	1040					
DB	531	GAATCAAAATCAAGTCTTTCTCTCGAACCATTCCGCAATGATGACACAGGCACTGCGCAT	590					

QY 1041 GCGGAGATCATCGACATCTCCAGTGGAACTGGGTGGGAACCCCTGGCAGCGACGATGA 1100  
DB 591 GGCAGACATCATCGAGTATTTCCGCTGGAACTGGGTGGGCAAAATGACGTGATGACGA 650  
QY 1101 CTATGGCCGCCAGGCAATGACAACTTCGGAGAGAGCGGTAAAGAGGACATCTGTAT 1160  
DB 651 CTATGGCCGCCAGGCAATGACAAATTCGGAGAGAGCGGTAAAGAGGATATCTGCAT 710  
QY 1161 TGACTTCAGTGAGATGATCTCTCAGTACTTACACCCAGAGAGTTGGAGTTTCATCGCCGA 1220  
DB 711 CGACTTCAGTGAGATGATCTCTCAGTACTTACACCCAGAGAGTTGGAGTTTCATCGCCGA 770  
QY 1221 CGTATCCAGAACTCTCCGGCCAAAGTATCATCTGGTCTCTTCCAAATGGCCCGACCTCGA 1280  
DB 771 GGTGATTCAAATTCACGCGCCAAAGTATCATCTGGTCTCTTCCAGTGGCCAGATCTTGA 830  
QY 1281 GCGCTATCCAGGAGATAGTTCCGAGAGAAATCAACCGATCGGATCTGGCTGGCCAGCGA 1340  
DB 831 GCGCTATCCAGGAGATAGTTCCGAGAGAAATCAACCGATCGGATCTGGCTGGCCAGCGA 890  
QY 1341 GCGTGGGCGAGCTCTTCGCTCATTCGCAAGCCAGAGTACTTCCACGTTGGTGGCGGCAC 1400  
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QY 1401 CATCGCTTCGCTCTAAGCGCGGCGGTATCCAGGGTTCAAAAGTTTCCTGAAGAGGT 1460  
DB 951 CATTCGATTCGCTCTAAGCGCTGGGCGAGATCCAGGCTTCGGGAATTCCTGAAGAGGT 1010  
QY 1461 CCACCCAGAGCTCTCGCAAGTGGTTCCTCAGAGTTCTCGGAGAGAGCTTCAAA 1520  
DB 1011 CCATCCAGAGAGTCTGTCCAAGTGGTTCCTCAGAGTTCTCGGAGAGAGCTTCAAA 1070  
QY 1521 CTGCTACTTTCACCGAGAGACCTCAGCGAGCTGAAGAAATTCAGAGTGCCTCGCAGG 1580  
DB 1071 CTGCACTCTCAAGA-----AGTGCMAAGACCTTTACCTGTGGACACCTTTCTG 1122  
QY 1581 ACGGCGGCTCAAGGGAGCGCTCAAGCGGGGAATTCAGCGGAGAGCGCTACGCA 1640  
DB 1123 AGAGG----TCAGAGAGAAAGTGGGACAGGTTTAGCAACAGCTCGACAGCTTCGAC 1178  
QY 1641 CCGCTGCACTGGGAGGAGAAATCAGCAGCGTGAGACCCCTACCTGGATTATACAA 1700  
DB 1179 CTTCTGTACAGGGATGAGAAATCAGCAGTGTGAGACCCCTTACATAGATTACAGCA 1238  
QY 1701 CTGAGGATCTCTCAATATAGTGGCCCTTACTCTCATTTGCTCAAGCCCTGCAAGA 1760  
DB 1239 TTTACGGATATCTCAATATAGTGGCCCTTACTCTCATTTGCTCAAGCCCTGCAAGA 1298  
QY 1761 CATCACTCTTCAAAACCGGACCGGATCTTTGCAAAAGGATCTTGTGAGATATTA 1820  
DB 1299 TATATATACCTCTTACCTGGAGAGGCTCTTACCAATGGCTCTGTGAGACATCAA 1358  
QY 1821 AAAAGTTAGGCTGGCAGGTCTCAACCATCTGCTGATCTGAAGTTTACCAAGCAT 1880  
DB 1359 GAAAGTTAGGCTGGCAGGTCTCAAGCACCTACGGCATCTAAATTTTCAAAATAT 1418  
QY 1881 GGTGAGAGGTTGATTTGATGATCAAGTGAACCTCAAGGGAGTACACCATATCAA 1940  
DB 1419 GGGGAGCAGGTGACCTTTGATGATGATGATGATGATGATGATGATGATGATGAT 1478  
QY 1941 CTGGAGCTCTCCGAGAGGATGAATCGGTGTTGTTTCCATAGGTGGGCAACTCAAGCC 2000  
DB 1479 CTGGACCTCTCCCGAGAGATGGCTCCATCGTGTGTTAAGGAGTCCGGTATTAAGT 1538  
QY 2001 CTACGCTAAGCCAGTACCGCATCAACATCAAGCAAGAAATCTCTGAGTGGCTT 2060  
DB 1539 CTATGCCAAGAGGAGAGAAAGTCTTTCATCAAGAGGAGAAATCTCTGAGTGGGT 1598  
QY 2061 CTCCAAAGTGGTCTCTTTCTCAACTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 2120  
DB 1599 CTCCAGGAGGTGCTCTCTCTCAACTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 1658

QY 2121 GATCATCGAGGGAGCCACCTGCTGCTTTGAATGATGGCATGTGCAGAGGAGT 2180  
DB 1659 GATCATTTGAGGGAGCCACCTGCTGCTTTGAGTGTGGAGTGTCTGATGGGAGTA 1718  
QY 2181 CAGTGATGAAAAAGTGAAGTGGTGTACAAAGTCCCGAATGATTTCTGTCTGATGA 2240  
DB 1719 TAGTGATGAGACAGATGCCAGTGCCTGTAAACAGTCCAGATGACTTTGTGTCATGA 1778  
QY 2241 GAAACACAGCTCTGATCGCCAAAGAGATCGAGTACTGTGCTGAGACGAGCCCTTCG 2300  
DB 1779 GAACCAACCTCTGATTTGCCAAGAGATCGAGTTTCTGTGTCGAGGAGCCCTTCG 1838  
QY 2301 GATGCTCTGACCATCTTGGCCCTATCGGCGATCTGATCACTCTTCTGTCTGGGGT 2360  
DB 1839 GATGCGACTCACCTCTTGGCGTGTGGGCAATTTCTCTGACAGCCCTTTGTGTGGTGT 1898  
QY 2361 CTTTCATCAGTTCCAGGAACACTCCATCGTGAAGGCCAACCCGGAGTTGCTTACCT 2420  
DB 1899 GTTTATCAGTTCCGCAACACACCTATGTCAAGGCCAACCCGAGAGCTCTCTTACT 1958  
QY 2421 GCTGCTCTTCTCTCTCATCTGTGCTTCTCCAGCTCGCTCATCTTTCATCGGAGCCAG 2480  
DB 1959 CTTCTCTTCTCTCTCTGCTGCTTCTCCAGCTCCCTGTTCTTTCATCGGAGCCCA 2018  
QY 2481 GGAATGACCTGTGCGCTCGGCCAACCGGCTTTGGCATCAGTTGCTCTGTGATCTC 2540  
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QY 2541 CTGCATCTGTGGAAGCAACCGGCTGTGCTGTGCTTTCGAGGCCAAGATCCCCACCA 2600  
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QY 2661 GGTGCAAACTGTCACCTGATCATCTGCTCTACACCGGCTCTCCCTCCAGCTACAGGA 2720  
DB 2199 CATGCAATGTCTGCTGTGATCTGCTCTACACCGGCTCTCCCTCCAGCTACAGGA 2258  
QY 2721 CCAATGAGTGGAGGACGAGTCTATCTTCACTGCTGCAAGGCTCTCTCATGCGCT 2780  
DB 2259 CCAGGAGTGGAGGATGAGATCATCTTCACTGCTGCAAGGCTCTCTCATGCGCT 2318  
QY 2781 GGGCTTCTCATCGGCTACACCTGCTCTCCCGGCTCTGCTTCTCTCTGCTTCTCTGCTTCAA 2840  
DB 2319 GGGCTTCTCATCGGCTACACCTGCTCTGCTGCTGCTGCTTCTCTCTGCTTCTCTGCTTCAA 2378  
QY 2841 GTCCGCTAAGTCTCCCGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTGAT 2900  
DB 2379 GTCCGCGAAGTCTCCCGAGAACTTCAATGAAGCAAGTTTCATCACCTTCAGCATGTGAT 2438  
QY 2901 CTTCTTCACTGCTGATCTCTTCACTCCCGGCTATGTCAGGACCTACGCGAGTGTGT 2960  
DB 2439 CTTCTTCACTGCTGATCTCTTCACTCCAGGCTATGTCAGGACCTATGCGAAGTGTGT 2498  
QY 2961 GTCCGCTGAGGCTGATTTGCTCTGCTCTCCAGTCTCCGCTCTGCTGCTGCTGCTGCTTAA 3020  
DB 2499 CTTCTGCTGAGGCTGATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTAA 2558  
QY 3021 CTTCAACAGTGTATCATCTGTTCAAGCGGCTGCTTAAACCATCATCGAGAGTGG 3080  
DB 2559 CTTCAACAGTGTATCATCTGTTCAAGCGGCTGCTTAAACCATCATCGAGAGTGG 2618  
QY 3081 CTTGAGAGCGGCGGCGGCTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3140  
DB 2619 TTTGAGAGCGGCGGCGGCTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2678  
QY 3141 CCGGCTCTGCAAGCGGCTCCAGGAGCTGTGCGGCTTCCACCATCTCTCTGCGGCTCTGCT 3200  
DB 2679 CGTCTCCCGCAAGCGGCTCCAGGAGCTTGGAGGCTCCAGGAGCTCCAGGAGCTCTCTCT 2738  
QY 3201 CACTGCGGCGGCGGCTCCACATGGAGATGAGCGCTGCAGCAGCAGAGAGGTGAGCTT 3260



QY 1341 GGCTGGGCGAGCTCTTCGCTCATTTGCCAAGCAGAGTACTTCCAGCTGGTGGCGGCAC 1400  
Db 1263 GGCTTGGGCGAGCTCTTCGCTCATTTGCCAAGCAGAGTACTTCCAGCTGGTGGCGGCAC 1322  
QY 1401 CATCGGCTTCGCTCTCAGGCGGGGGGTATCCAGGGTTCAACAAGTTCTCCTGAAGAGGT 1460  
Db 1323 CATGGATTGCTCTGAAGGCTGGGCAGATCCAGGCTTCGGGAATTCCTGAAGAGGT 1382  
QY 1461 CACCCCGAGAGTCTCTCGCAAAATGGGTTTGTCAAGAGTTCTGGGAGGACCTTCAA 1520  
Db 1383 CCATCCAGAGAGTCTGTCCAAATGGTTTTCGAAGGAGTTTGGGAGAAACATTTAA 1442  
QY 1521 CTGTACTTCCAGGAGAGACCTGACGAGCTGAAGAAATTCGAAGTGGCTCCGACGG 1580  
Db 1443 CTGCCACCTCCAGA-----AGTGCAAGAGACCTTTACCTGTGGACACCTTTCTG 1494  
QY 1581 ACCGGCGGTCAAGGGGAGCGGTCCAGAGCGGGGAACTCCAGACGAGAGCTTACGCCA 1640  
Db 1495 AGAGG----TCACGAAGAAAGTGGGCACAGGTTTACCAACAGCTCGACAGCCTTCGGACC 1550  
QY 1641 CCCTGCACTGGGGAGGAGAAATCACAGCGTGGAGACCCCTACCTGGATTATACACA 1700  
Db 1551 CCTCTGTACAGGGGATGAGAAATCAGCAGTGTGAGACCCCTTACATAGATTACAGCA 1610  
QY 1701 CCTGAGGATCTCTCAATGTATAGTGGCGGTCTACTCTCATTTGCTCACGCCCTGCAAGA 1760  
Db 1611 TTATAGGATATCTCAATGTGTACTTAGCAGTCTACTCCATTGGCCACGCTTGCAGA 1670  
QY 1761 CATCACTCTTGAACCCGCGACGGGATCTTTCGAACGATCTTGTGAGATTTAA 1820  
Db 1671 TATATATCTCTTACCTGGGAGAGGCTCTTCAACCAATGGCTCCTGTGACAGATCAA 1730  
QY 1821 AAAAGTTGAGGCTGGCAGGCTCTCAACCATCTGTGATCTGAAGTTTACCAACAGCAT 1880  
Db 1731 GAAAGTTGAGGCTGGCAGGCTCTGAGCACCTACGGGATCTAACTTTACAAACAATAT 1790  
QY 1881 GGGTAGCAGGTTGATTTGACGATCAAGGTGACCTCAAGGGGAACTACCATTTATCAA 1940  
Db 1791 GGGGAGCAGGTTGACCTTTGATGAGTGTGTGACCTGGTGGGAACTATTTCATCATCAA 1850  
QY 1941 CTGGCAGCTCTCCGACAGAGATGAATCGGTGTGTTCCATGAGTGGGCAACTACAGCG 2000  
Db 1851 CTGGCACCTCTCCACAGAGATGGTCCATCGTGTAAAGAGTGGGGTATTACAGCT 1910  
QY 2001 CTACGCTAAGCCAGTGCAGCTCAACATCAACAGAAAGAAATCTCTGAGTGGGTT 2060  
Db 1911 CTATGCCAAGAGGAGAAAGACTCTTCAATCAACAGGAGAAATCTCTGTGGAGTGGGTT 1970  
QY 2061 CTCCAAAGTGGTTCCTTTCTCAATGCGAGTGCAGACTGTGCGCGGCACCCAGGAAGG 2120  
Db 1971 CTCGAGGAGGTGCCCCCTCTCAACTGCGAGCGAGACTGCTGGCAGGACCCAGGAAGG 2030  
QY 2121 GATCATCGAGGGGAGGCCACCTGCTGCTTTGAATGCAATGCGCATGTGACAGGAGAGTT 2180  
Db 2031 GATCATTTGAGGGGAGGCCACCTGCTGCTTTGAGTGTGTGGAGTGTCTGTATGGGAGTA 2090  
QY 2181 CAGTGTAAAGAGTGAAGTGTGTACAAAGTGCAGGATGATTTCTGTCGAATGA 2240  
Db 2091 TAGTGATGAGACAGATGCGCAGTGAACAGTGCAGGATGATTTCTGTCGAATGA 2150  
QY 2241 GAACACACGCTGCTGATCGCAAGAGATCAGTACCTGTCTGGAGCGAGCCCTTCGG 2300  
Db 2151 GAACACACCTCTCTGATTTGCCAAGAGATCAGTGTCTGTGTGAGCGAGGCCCTTTGG 2210  
QY 2301 GATGCTCTGAACAATCTTCGCGTACTGGGCATCTCTGATACCTCTTCTGCTGGGGGT 2360  
Db 2211 GATGCACTACACCTCTTTCGCGGTGTGGGCATTTCTCTGACAGCCTTTGTGCTGGGTGT 2270  
QY 2361 CTTTCAATGATTCAGGAACACTCCCATCGTGAAGGCCACCAACCGGGAGTTGTCTACTCT 2420  
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QY 2421 GCTGCTCTTCTCCCTCATCTGCTGCTTCTTCCAGCTCGCTCATCTTTATCGGAGGCCAG 2480

Db 2331 CTTCTCTTCTCCTGCTGCTGCTTCTTCCAGTCCCTGTTCTTTCATCGGAGGCCCA 2390  
QY 2481 GGAAGTGAACCTGTGCGGTCCGCCAAACGGGCTTTGGATCAGCTTGTCTGTGCAATCTC 2540  
Db 2391 GGAAGTGAACCTGTGCGGTCCGCCAAACGGGCTTTGGATCAGCTTGTCTGTGCAATCTC 2450  
QY 2541 CTTGATCCTGCTGAAGACCAACCGGCTGTGCTGCTTTCAGGCAAGATCCCAACCAAG 2600  
Db 2451 ATGATCCTGCTGAAGACCAACCGGCTGTGCTTCTTCTGCTTGTGAGGCCAAGATCCCAACCAAG 2510  
QY 2601 CTTCCACCGCAAGTGGGTGGGCTCAACCTGCAAGTTCCTCTGCTGCTTCTCTGCAATCT 2660  
Db 2511 CTTCCACCGCAAGTGGGTGGGCTCAACCTGCAAGTTCCTCTGCTGCTTCTCTGCAATCT 2570  
QY 2661 GGTGCAATCTGACCTGATCATCTGGCTCTACACGGGCTCCCTCCAGCTACAGGA 2720  
Db 2571 CATGCAATTTGATCTGTGATCTGGCTCTACACGGGCTCCCTCAAGCTACCGCA 2630  
QY 2721 CCATGAGCTGGAGGAGAGTCTATCTTCACTGCACTGCGAGAGGCTCGCTCATGGCGCT 2780  
Db 2631 CCAGGAGCTGGAGGATGAGATCATCTTCACTGCTGCCAGAGGCTCTCCTCATGGCCT 2690  
QY 2781 GGGCTTCTCATCGGCTACACCTGCTCTCTGCGGCTATCTGCTTCTTCTGCTTCTCA 2840  
Db 2691 GGGCTTCTCATCGGCTACACCTGCTGCTGCTGCTGCTTCTTCTTCTTCTGCTTCTCA 2750  
QY 2841 GTCCGCTAAGCTCCCGAGAACTTCAACGAGGCTAAGTTTCACTGCTTCACTGCTTCA 2900  
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QY 2961 GTGGCGGTGGAGTGTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCT 3020  
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QY 3021 CTTCAACAAGTGTATCATCTCTTCAAGCGCTGCTTCACTGCTTCACTGCTTCACTGCT 3080  
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QY 3081 CTGAGCAAGCGGCGGCGGCTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3140  
Db 2991 TTGAGCAAGCGGCGGCGGCTTCAAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 3050  
QY 3141 CCGCTTCTCGCAAGCGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCT 3200  
Db 3051 CCGTCTCGGAGAGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCT 3110  
QY 3201 CACCTGCGGCGGCGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCT 3260  
Db 3111 CATGAGCAAGAGCAAGCA-----GCGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 3165  
QY 3261 CCGAGCGGCGGCGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCT 3320  
Db 3166 CAGAGCGGCGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCT 3225  
QY 3321 CAGCGCGGCGGCGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCTTCAAGTGGGCGGCT 3382  
Db 3226 CAGCAGCAAGTGTCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3267

RESULT 13  
ABX74489  
ID ABX74489 standard; cDNA; 3783 BP.  
XX  
AC ABX74489;  
XX  
DT 21-MAR-2003 (first entry)  
XX  
DE Human cDNA sequence #32 down-regulated in CC-RCC patients.









2091	DB	TAGTGAAGAGACAGATGCCAGTGCCTGTAAACAAGTGCCACAGATGAATTCTGTGTCCAAATGA	2155
2241	QY	GAACCAACACGCTCGTGCATCGCCAAAGAGATCGAGTACTGTCGTGACGAGAGCCCTTCGG	2300
2151	DB	GAACCAACACCTCTGCAATCGCAAGGAGATCGAGTTTCTGCTGAGCAGAGCCCTTTGG	2210
2301	QY	GATCGCTTGACCAATCTTTCGCGTACTGGGCATCTTGATCACCTCCTTCTGTCGTGGGGT	2360
2211	DB	GATCGCACTCACCCCTCTTTTCGCGTGTGGCAATTTTCTGACAGCCCTTTGTGTGGGTGT	2270
2361	QY	CTTCATCAAGTTTCAGGAACACTCCCATCTGTGAAGGCCAACCAACGGGAGTTGTCTTACCT	2420
2271	DB	GTTTATCAAGTTTCGCAACACACCCATTGTCAAGGCCAACCAACGAGAGCTCTCTTACCT	2330
2421	QY	GCTGCTCTTCTCCCTCAATCTGCTCTTCTCCAGCTCGCTCATCTTCAATCGCGAGGCCAG	2480
2331	DB	CCTCCTCTTCTCCCTGCTCTGCTGCTTCTCCAGCTCCCTCTTCTCATCGGGAGAGCCCA	2390
2481	QY	GGACTGACCTGTGCGCTCGCCAAACGGGCTTTGGCATCAGGTTGTCGTCGTGCAATCTC	2540
2391	DB	GGACTGACGTGCGCTCTGCGCACGCGGCTTTGGCATCAGGTTGTCGTCGTGCAATCTC	2450
2541	QY	CTGCATCCTGGTGAAGACCAACCGGCTGTCTGTCTTCAGAGCCAAAGATCCCAACCAG	2600
2451	DB	ATGCATCCTGGTGAACCAACACCGTGTCTCTCTGGTGTGAGGCCAAGATCCCAACCAG	2510
2601	QY	CCTCCACCGCAAGTGGGTGGGCTCAACCTGCAATGCTCTCTCGTCTTCTCTCTGCAATCTC	2660
2511	DB	CTTCCACCGCAAGTGGGTGGGCTCAACCTGCAATGCTCTCTCGTCTTCTCTCTGCAATCTC	2570
2661	QY	GGTGCAAATCGTCACCTTGCAATCATCTGGCTCTACACGCGCCCTCCCTCCAGCTACAGGA	2720
2571	DB	CATGCAGATTGTCAATCTGTGTGATCTGGCTCTACACGCGCCCTCCAGCTACAGCA	2630
2721	QY	CCATGAGCTGGAGGACGAGGTCAATCTTCATCACTCTGGAGAGGGCTCGCTCATGGGCT	2780
2631	DB	CCAGGAGCTGGAGGATGAGATCAATCTTCATCAGTGCACGAGGGCTCCCTCATGGCCCT	2690
2781	QY	GGGCTTCTCATCGGCTACACCTCGCTCTCGCGCCATCTGCTCTTCTTTCGCCCTCAA	2840
2691	DB	GGGCTTCTCATCGGCTACACCTCGCTCTCGCGCCATCTGCTCTTCTTTCGCCCTCAA	2750
2841	QY	GTCCGTPAAGCTGCCGGAACCTTCAACGAGGCTAAGTTCAATCACCTTCAGCANGTTGAT	2900
2751	DB	GTCCGGAAGCTGCCGGAACCTTCAATGAAGCCAAAGTTCAATCACCTTCAGCANGTTGAT	2810
2901	QY	CTTCTTCATCGTCTGGATCTTCCTTCATCCCGGCTATGTCAGACACTACGGCAAGTTGT	2960
2811	DB	CTTCTTCATCGTCTGGATCTTCCTTCATCCCGGCTATGTCAGACACTACGGCAAGTTGT	2870
2961	QY	GTGGCGCTGGAGGTGATTGCCATCTTGGCTCCAGCTTCGGGCTGCTGGGCTGCAATTA	3020
2871	DB	CTTGGCGTAGAGGTGATTGCCATCTTGGCAGCCAGCTTTTGGTTGCTGGCGTGCACTTT	2930
3021	QY	CTTCAACAAGTTTACATCATCTGTTCAAGCGTGCCGTAAACACCATCAGAGAGTGCG	3080
2931	DB	CTTCAACAAGATCTACATCAATCTTTCAGACCAATCCCGCAACCAATCAGAGAGTGCG	2990
3081	QY	CTGCAGACGCGGCCACACGCTTCAAGGTGGGGGCCCGGGCCACCCCTCCGGCGCAGCGC	3140
2991	DB	TTTCAGACACCGAGCTCACGCTTTCAGAGTGCGTGTCCCGGCCACGCTGCGCGCAGCAA	3050
3141	QY	CGGCTCTCGAAGCGCTTCAAGAGCTGTGCGGCTTCAACCATCTCTGCGCCGCTCGTC	3200
3051	DB	CGTCTCCGCAAGCGGCTTCAGAGCCTTTGAGGCTTCCACGGGATCCACCCCTCTCTCTC	3110
3201	QY	CACCTGGGCGCGGCTCTCCATGGAGATGACGCGCTGCAGACGCGAGAAGTGCAGCTT	3260
3111	DB	CATCAGACGACGAGCAACA-----GCAGAACCATTTCCACAGCCGAGAGGCAGAG	3165
3261	QY	CGGACGCGGACCGGTCAACCTGTGTGCTCAGCTTCGAGGAGACAGGCCGATACGCCACCTT	3320
3166	DB	CAGCAGCAGCGCTTGGGCTTAAACCCAGCAAGAGCAGCAGCAGCGCCCTTGAACCTTCCCA	3225

Qy	3321	CAGCCGACGGCCGAGCAGGAGAACTCGCGGATGCGCGAG	3362
Db	3226	CAGCAGCAAGATCTCTCAGCAGCAGCCAGATCAAGCAGAAG	3267
RESULT 15			
AAV26964	AAV26964 standard; cDNA to mRNA; 3809 BP.		
AC	XX	AC	AAV26964;
XX	XX	XX	01-SEP-1998 (first entry)
DT	XX	XX	Human parathyroid calcium receptor 4.0 gene 4Kb fragment.
DE	XX	XX	ss; calcium ion concentration; parathyroid hormone; homeostasis; kidney;
KW	XX	XX	calcium receptor; detection.
KW	XX	XX	Homo sapiens.
OS	XX	XX	
XX	XX	XX	Key
FH	XX	XX	Location/Qualifiers
FT	XX	XX	373..3609
FT	XX	XX	/tag= a
FT	XX	XX	/product= "pHuPCar 4.0 4Kb fragment"
XX	XX	XX	US5763569-A.
PN	XX	XX	
XX	XX	XX	09-JUN-1998.
PD	XX	XX	
XX	XX	XX	07-JUN-1995; 95US-00484565.
XX	XX	XX	23-AUG-1991; 91US-00749451.
PR	XX	XX	11-FEB-1992; 92US-00834044.
PR	XX	XX	21-AUG-1992; 92US-00934161.
PR	XX	XX	12-FEB-1993; 93US-00017127.
PR	XX	XX	23-FEB-1993; 93US-00009389.
PR	XX	XX	22-OCT-1993; 93US-00141248.
PR	XX	XX	19-AUG-1994; 94US-00292827.
PR	XX	XX	21-OCT-1994; 94WO-US012117.
XX	XX	XX	08-DEC-1994; 94US-00353784.
XX	XX	XX	(NPSP-) NPS PHARM INC.
PA	XX	XX	(SGHM ) BRIGHAM & WOMENS HOSPITAL.
PI	XX	XX	Hebert SC, Brown EM, Garrett JE;
PI	XX	XX	
DR	XX	XX	WPI; 1998-347412/30.
DR	XX	XX	P-FSDB; AAW54846.
XX	XX	XX	
FT	XX	XX	Calcium receptor poly:peptide(s) - useful for drug screening or antibody
PT	XX	XX	production.
XX	XX	XX	
PS	XX	XX	Example 27; Fig 49; 174pp; English.
XX	XX	XX	The Human parathyroid calcium receptor gene encodes a 1078 amino acid
CC	XX	XX	protein. The tissue from which the receptor and receptors from bovine
CC	XX	XX	parathyroid and rat kidney are derived, respond to changes, and control
CC	XX	XX	changes, in calcium ion concentration, e.g. parathyroid hormone regulate
CC	XX	XX	Ca2+ homeostasis in blood and extracellular fluid, and kidney function
CC	XX	XX	alters through changes in Ca2+ levels in juxtaglomerular and proximal
CC	XX	XX	tubule cells in the kidney. The purified receptors (produced
CC	XX	XX	recombinantly) can be used to screen for compounds that modulate calcium
CC	XX	XX	receptor activity, especially those that can be used to treat diseases
CC	XX	XX	associated with the receptors in these tissues. They can also be used to
CC	XX	XX	raise antibodies for use in detection assays
XX	XX	XX	
XX	XX	XX	Sequence 3809 BP; 910 A; 1071 C; 979 G; 849 T; 0 U; 0 Other;
XX	XX	XX	
XX	XX	XX	Query Match 42.2%; Score 1745.2; DB 2; Length 3809;
XX	XX	XX	Best Local Similarity 76.4%; Pred. No. 6e-300;
XX	XX	XX	Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps

QY 501 CTCAGGATATGTCTCAAAACCAAGGCGCCAGAGAAAGAGACATCATCTACTGGAGGTCT 560  
DB 423 CTCTGCTACTACGGGCCAGACCCAGCAGCGCCCAAGAGGGGACATTAATCTTGGGGGCT 482  
QY 561 CTTCCCAATACACTTTGGAGTAGCGCCCAAGGATCAGGACTTAAATCGAGACCGAGGC 620  
DB 483 CTTTCTCTATCAATTTGGAGTAGAGCTAAGATCAGATCTCAATCAAGCCGGAGTC 542  
QY 621 GACAAAATGATTCGGTCAAAATTTTCGAGGCTTCGATGGCTCCAGGCGATGATATCGC 680  
DB 543 TGTGGAATGATACAGGTATAATTCGTGGGTTTCGTGGTTACAGGCTATGATATTTGC 602  
QY 681 RAATCGAGAGATTAAACAGATACACTTTCTGCGCCCAATATCACTCCGATTCGCAT 740  
DB 603 CATAGAGAGATAAACAGAGCCCGACCTCTTCCCACTTTGACGCTGGGATCAGGAT 662  
QY 741 ATTTGACACGCTTAACACCGTGTCCAAGCGCTAGAGGCAACACTCAGCTTTGTGGCCCA 800  
DB 663 ATTTGACACTTCCAAACACCGTTCTAAGGCTTTGAAGCCACCTCGAGTTTGTGCTCA 722  
QY 801 GAACAAATCGACTCGTGAACCTTAGATGAGTTCTGTAACCTGCTGACCATATCCCATC 860  
DB 723 AAAACAAATATGATTTTGAACCTTTGATGAGTTCTGCAACTGCTCAGAGCAATCCCTC 782  
QY 861 CACAATAGCAGTGTGCGGGCAACCGGCTCAGGAATCTCCAGGCTGTGGCAATCTATT 920  
DB 783 TAGGATGCTGTGGTGGAGCACTGGCTCAGGCTCTCCAGCGAGTGGCAATCTGCT 842  
QY 921 GGGATATTTTACATTCACAGGTGAGCTATGCTCTCTCGAGCGGCTGCTCAGCAACA 980  
DB 843 GGGGCTCTTACATTCGCCAGGTGAGTTATGCTCTCCAGGAGACTCTCAGCAACA 902  
QY 981 GAATGAGTACAGGCTTCTTGAGGACCATCCCAATGATGAGCAACAGGCGCCGCT 1040  
DB 903 GAATCAATCAAGTCTTTCTCCGAACCATCCCAATGATGAGCAACAGGCGCTGCT 962  
QY 1041 GSCGAGATCATCGACACTTCCAGTGGAACTGGGTGGGAACTCCCTGGCAGCGCAGATGA 1100  
DB 963 GGCAGACATCATCGAGTATTTCCGCTGGAACTGGGTGGGCAATTCGAGCTGATGAGA 1022  
QY 1101 CTATCGCGCCAGGATGACAAAGTTCCGGAGGAGCGGTTAAGAGGACATCTGTAT 1160  
DB 1023 CTATCGCGCGCGGGATTGGAATTCGAGAGGAAGCTGAGGAAAGGATATCTGCAT 1082  
QY 1161 TGACTTCAGTGAATGATCTCTCAGTACTACACCCAGAAAGAGTTGGAGTTCTATCGCGCA 1220  
DB 1083 GCACTTCAGTGAATCATCTCCAGTACTCTGATGAGGAGNGATCCAGCATGTGTAGA 1142  
QY 1221 GCTCATCAGAACTCTCTCGGCCAAGGTATGCTGTGCTTCTCCAAATGCGCCCGACCTGGA 1280  
DB 1143 GGTGATCAAAATTCACCGGCCAAAGTATCGTGTGTTTTCTCCAGTGGCCAGATCTTGA 1202  
QY 1281 GCGGCTCATCCAGGAGATGTTCCGAGAAACATACCCGATCGGATCTGCTGGCCAGGGA 1340  
DB 1203 GCGCTCATCAGGAGATTTCCGGCGCAATATCAGGGGCAAGATCTGCTGGCCAGGGA 1262  
QY 1341 GGCCTGGGCGAGCTCTCTCCATTTGCCAAGCAGAGTACTTCCACGTGGTTCGCGGCAC 1400  
DB 1263 GGCCTGGGCGAGCTCTCTCCATGATCGCATGCTCAGTACTTCCACGTGGTTCGCGGCAC 1322  
QY 1401 CATCGGCTCTCTCAGGGCGGGGCTATCCAGGTTTCAACAGTTCTCTGAAGAGGT 1460  
DB 1323 CATTGATTCGCTCTGAAGGCTGGGAGATCCAGGCTTCCGGGAATTCCTGAAGAGGT 1382  
QY 1461 CCACCCCGAGAGCTCTCGCAATGGGTTTCTCAAGAGTTCTGGGAGGAGACTTCAA 1520  
DB 1383 CCATCCCGAGGATCTGTCCCAATGTTTTCGCAAGGATTTTGGGAAGAAACATTTAA 1442  
QY 1521 CTGCTACTTCCAGGAAGA CCGTGAAGAGCTGAAGAAATTCGAAGTGGCCCTCGCAGG 1580  
DB 1443 CTGCCACCTTCCAAGA-----AGGTCAAAAGAGACCTTTTACCTGTGGACACCTTTCTG 1494  
QY 1581 ACCGGCGCTCAAGGGAGCGGCTCCAAGCGGGGAACTCCAGACGAGCCCTACGCCA 1640

DB 1495 AGAGG-----TCACGAAGAAAGTGGCGACAGGTTTAGCAACAGCTCAGACGCTTCGACC 1550  
QY 1641 CCGCTGACCTGGGAGGAGAAACATCACCAGCGTGGAGAGCCCCCTACTGGAATATACACA 1700  
DB 1551 CTTCTGTACAGGGGATGAGAAACATCAGAGTGTGAGAGCCCCCTTACATAGATTACAGCA 1610  
QY 1701 CTTGAGGATCTCTACAAATGATACGTGGCGCTCTACTCTCATTTGCTCAGCCCTGCAAGA 1760  
DB 1611 TTTACGGATATCTTACAAATGTACTTAGCAGTCTACTCCATTCGCCCGCTTGAAGA 1670  
QY 1761 CATCCACTCTTGCAAAACCCGCGACGGCATCTTTGCAAAACGGATCTTGTGCAGATTTAA 1820  
DB 1671 TATATATACCTGTACTTACCTGGAGAGGGCTCTTCACAATGGCTCTCTGTCAGACATCAA 1730  
QY 1821 AAAAGTTGAGCGCTGGCAGGCTCTCAACCATCTGCTGCATCTGAAAGTTTACCAACAGCAT 1880  
DB 1731 GAAAGTTGAGCGCTGGCAGGCTCTGAAGCACCTACGCGCATCTAACTTTACAAACAATAT 1790  
QY 1881 GGGTGAAGAGTTGACTTTTGAACGATCAAGGTGACCTCAAGGGGAACTACACCAATTTCAA 1940  
DB 1791 GGGGAGCAGGTGACCTTTGATGAGTGTGTGACCTGGTGGGAACTATTTCCATCATCAA 1850  
QY 1941 CTGCGAGCTCTCCGCGAGAGATGAATCGGTGTTTTCATGAGTGGGCGCAACTACAACGC 2000  
DB 1851 CTGCGACTCTCCCGAGAGGATGCTCCATCGTGTGTTAAGGNAAGTCGGGTATTTACAACGT 1910  
QY 2001 CTAGCTAAGCCAGTGAACGACTCAACATCAACGAAGAAATAATCTCTGGAGTGGCTT 2060  
DB 1911 CTATGCCAAGAGGAGAAAGACTCTTCACTCAACGAGGAGAAATACTCTGTGGAGTGGTT 1970  
QY 2061 CTCGAAAGTGGTTCTTTCTCCAACTGCGAGTCCAGACTGTGCGCGGCGACCGAGGAGGG 2120  
DB 1971 CTCGAGGAGTGGCTTTCTCCAACTGCGAGCGAGACTGCTGGCAGGAGNCCAGGAAAG 2030  
QY 2121 GATCATGAGGGGAGCCCACTGCTGCTTTTGAATGATGGCATGTGCGAGAGGAGGAT 2180  
DB 2031 GATCAITAGGGGAGGCCACCTGCTGCTTTGAGTGTGGAGTGTCTGATGGGAGTA 2090  
QY 2181 CAGTGATGAAACGATGCAAGTGGGTGTACAAAGTCCCGAATGATTTCTGTCGAATGA 2240  
DB 2091 TAGTGATGAGACAGATGCCAGTGCCTGTAAAGTGGCCAGATGACTTCTGGTCCCAATGA 2150  
QY 2241 GAACCAACAGCTCTGTCATCGCCAAAGAGATCGAGTACCTGTCTGCGAGCGAGCCCTTCGG 2300  
DB 2151 GAACCAACAGCTCTGTCATTCGCAAGGAGATCGAGTTTCTGTCGTCGAGCGAGCCCTTGG 2210  
QY 2301 GATCGCTCTGACCATCTTTCGCGCTACTGGGCTCTGATCACTCTCTTGTGCTGGGGT 2360  
DB 2211 GATCGCACTCACCTCTTTTCGCGCTGTCGGGCATTTTCTGACAGCCCTTTGTGCTGGGTGT 2270  
QY 2361 CTTTCACTCAAGTTCAGGAACACTCCCATCGTGAAGGCGCACCAACCGGGAGTTGTCTACCT 2420  
DB 2271 GTTTATCAAGTTCGCAACACACCAATGTCAAGGCGCACCAACCGAGAGCTCTCTACCT 2330  
QY 2421 GCTGCTCTTCTCCCTCATCTGCTGCTTCTCAGCTCGCTCATCTTTCATCGGCGAGCCAG 2480  
DB 2331 CTTCTCTTCTGCTGCTGCTGCTTCTCAGCTCCCTGTTCTTCTATCGGGAGGCCCA 2390  
QY 2481 GGAATGAGCTGTGCGCTCGCCCAACCGGCTTTTGGCATCAGCTTCTGCTGTGCAATCTC 2540  
DB 2391 GGAATGAGCTGTGCGCTCGCCCGAGCGGCTTTTGGCATCAGCTTCTGCTGTGCAATCTC 2450  
QY 2541 CTGCATCTCTGGTGAAGACCAACCGGGTGTGCTGTGTCTTCGAGGCGCAAGATCCCCACAG 2600  
DB 2451 ATGCATCTCTGGTGAAGAACCAACCGGTGTCTCTCTGGTGTGGAGGCAAGATCCCCACAG 2510  
QY 2601 CTTCCACCGAAGTGGGTGGGCTCAACCTGAGATTTCTCTGGTCTTCTCTGCAATCTC 2660  
DB 2511 CTTCCACCGAAGTGGGTGGGCTCAACCTGAGTTCCTGCTGTTTCTCTGCACTT 2570  
QY 2661 GGTGCAATCGTCACTGCAATCATCTGGCTCTACACGCGGCTCTCCCTCAGAGCTACAGGAA 2720



Db	2571	CATGACAGATTGTCATCTGTGTGATCTGGCTCTACACCGCGCCGCCCTCAAGCTACCGCAA	2630
Qy	2721	CGATGAGCTGGAGGAGGAGGTCATCTTTCATACCTGCGACGAGGAGGCTCGCTCATGGCGCT	2780
Db	2631	CCAGGAGCTGGAGGATGAGATCATCTTCATACGTGCGACGAGGAGCTCCCTCATGGCCCT	2690
Qy	2781	GGGCTTCTCTCATCGGCTACACCTGCTCTCTCGCCGCCATCTGCTTCTTCTTGGCTTCAA	2840
Db	2691	GGGCTTCTCTGATCGGCTACACCTGCTCTGCTGCTGCCATCTGCTTCTTCTTGGCTTCAA	2750
Qy	2841	GTCCCGTAAGCTGCCGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTTGAT	2900
Db	2751	GTCCCGTAAGCTGCCGAGAACTTCAATGAGCCAAAGTTTCATCACCTTCAGCATGTTGAT	2810
Qy	2901	CTTCTTCATCTGCTGTGATCTCTCTTCATCCCGCCCTATGTACGACCTACGGCAAGTTTGT	2960
Db	2811	CTTCTTCATCTGCTGTGATCTCTCTTCATCCAGCCCTATGCCAGCCTATGGCAAGTTTGT	2870
Qy	2961	GTCCGCGTGGAGGATGATGCCATCTGSCCTCCAGCTTCGGGCTGCTGGGCTGCATTTA	3020
Db	2871	CTCTGCGTAGAGGTCATGCCATCTGCGACCCAGCTTTGGCTTGGCTGGCTGCATCTT	2930
Qy	3021	CTTCAACAAGTGTATCATCTCTGTTCAGGCGGTGCGTAAACACCATCGAGGAGTGCG	3080
Db	2931	CTTCAACAAGTGTATCATCTCTGTTCAGGCGATCCCGCAACACCATCGAGGAGTGCG	2990
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Db	2991	TTGCAGCACCGCAGCTCACGCTTTCAGGTGGCTGCCGGGCGACGCTGGCGCGCAGCAA	3050
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Qy	3201	CACCTCGGGCGGGGCTCACCATGGAGATGAGGCTGCGAGCAGCAGAGAGGTGAGCTT	3260
Db	3111	CATCAGCAGCAAGAGCAACA----GCGAAGACCCATTCCACAGCCCGAGAGGCGAGAAG	3165
Qy	3261	CGGAGCGGCGACGCTCACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3320
Db	3166	CAGCAGCAGCGCTGGCCCTTAACCCAGCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGC	3225
Qy	3321	CAGCGCAGCGCGCGCAGCAGGAACTCGGGCGGATGGCGCGAG	3362
Db	3226	CAGCAGCAACGATCTCAGCAGCAGCCAGATGCAAGCAGAAG	3267

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Job time : 1831 secs

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 22:20:13 ; Search time 317 Seconds  
(without alignments)  
9269.405 Million cell updates/sec

Title: US-10-016-496-1

Perfect score: 4134

Sequence: 1 aattccgttctgtcgttc.....aagcgccgacagcaacgg 4134

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.NA.\*

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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
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6: /cgn2\_6/ptodata/1/ina/backfiles.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4134	100.0	4134	3	US-09-162-021B-1
2	4134	100.0	4134	4	US-09-687-477-17
3	4134	100.0	4134	4	US-09-687-476-17
4	4134	100.0	4134	4	US-09-687-372-17
5	4134	100.0	4134	4	US-09-975-553-17
6	4134	100.0	4134	4	US-10-270-795-17
7	4134	100.0	4134	4	US-10-270-876-17
8	4134	100.0	4134	4	US-10-268-051-7
9	1745.2	42.2	3809	1	US-08-485-588-3
10	1745.2	42.2	3809	1	US-08-484-585-3
11	1745.2	42.2	3809	2	US-08-480-751-3
12	1745.2	42.2	3809	2	US-08-943-986-3
13	1745.2	42.2	3809	3	US-08-353-784-3
14	1745.2	42.2	3809	3	US-08-484-719B-3
15	1745.2	42.2	3809	3	US-08-546-998-2
16	1745.2	42.2	3809	3	US-08-484-159-3
17	1743.6	42.2	3234	4	US-09-016-434-1432
18	1738	42.0	5275	1	US-08-485-588-1
19	1738	42.0	5275	1	US-08-484-565-1
20	1738	42.0	5275	2	US-08-480-751-1
21	1738	42.0	5275	2	US-08-943-986-1
22	1738	42.0	5275	3	US-08-353-784-1
23	1738	42.0	5275	3	US-08-484-719B-1
24	1738	42.0	5006	1	US-08-485-588-2
25	1703.6	41.2	5006	1	US-08-484-565-2
26	1703.6	41.2	5006	2	US-08-480-751-2
27	1703.6	41.2	5006	2	US-08-480-751-2

28 1703.6 41.2 5006 2 US-08-943-986-2 Sequence 2, Appli  
29 1703.6 41.2 5006 3 US-08-353-784-2 Sequence 2, Appli  
30 1703.6 41.2 5006 3 US-08-484-719B-2 Sequence 2, Appli  
31 1703.6 41.2 5006 3 US-08-546-998-1 Sequence 1, Appli  
32 1703.6 41.2 5006 3 US-08-484-159-2 Sequence 1, Appli  
33 1681.6 40.7 3173 3 US-09-134-513-1 Sequence 1, Appli  
34 1678.2 40.6 4131 1 US-08-485-588-4 Sequence 4, Appli  
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39 1678.2 40.6 4131 3 US-08-484-719B-4 Sequence 4, Appli  
40 1678.2 40.6 4131 3 US-08-484-159-4 Sequence 4, Appli  
41 1123.6 27.2 4000 2 US-08-687-289A-2 Sequence 2, Appli  
42 1123.6 27.2 4000 4 US-09-435-897-2 Sequence 2, Appli  
43 1111.4 26.9 2925 4 US-09-695-481-3 Sequence 3, Appli  
44 849.6 20.6 2148 5 PCT-US93-01642-1 Sequence 1, Appli  
45 711.8 17.2 3384 2 US-08-687-289A-1 Sequence 1, Appli

#### ALIGNMENTS

RESULT 1  
US-09-162-021B-1  
; Sequence 1, Application US/09162021B  
; Patent No. 6337391  
; GENERAL INFORMATION:  
; APPLICANT: H. William Harris  
; APPLICANT: Edward M. Brown  
; APPLICANT: Steven C. Hebert  
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic  
; TITLE OF INVENTION: Species and Methods of Use Thereof  
; FILE REFERENCE: 2856.1001-007  
; CURRENT APPLICATION NUMBER: US/09/162,021B  
; CURRENT FILING DATE: 1998-09-28  
; PRIOR APPLICATION NUMBER: PCT/US97/05031  
; PRIOR FILING DATE: 1997-03-27  
; PRIOR APPLICATION NUMBER: 08/622,738  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 4134  
; TYPE: DNA  
; ORGANISM: squalus acanthias  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (439)...(3522)  
US-09-162-021B-1

Query Match 100.0%; Score 4134; DB 3; Length 4134;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 AATTCGTTGCTCTCGGTTCCAGTCTCTCCAGTGCAAAATGAGAAATGGTGGTC 60  
Qy 61 GCATATACAGAAATGCATCATCTGTGTTAATGAAATATTTGTCAGTTATCTGAAGT 120  
Db 61 GCATATACAGAAATGCATCATCTGTGTTAATGAAATATTTGTCAGTTATCTGAAGT 120  
Qy 121 TATTAATAATTTTCTCAAGATGGCTTTCAGGAAATCAATTTCTCAGCTTTTCCATT 180  
Db 121 TATTAATAATTTTCTCAAGATGGCTTTCAGGAAATCAATTTCTCAGCTTTTCCATT 180  
Qy 181 GTCAATGTATGAATACTGCCAAAGGATGAACAAATGGAACAAAGCTGAGGACCAC 240  
Db 181 GTCAATGTATGAATACTGCCAAAGGATGAACAAATGGAACAAAGCTGAGGACCAC 240  
Qy 241 GTTCAACCTTTCTTGGAGCATCGATCAACCTTGAAGGAGATGGAAGACTTGAAGGAA 300  
Db 241 GTTCAACCTTTCTTGGAGCATCGATCAACCTTGAAGGAGATGGAAGACTTGAAGGAA 300

Db 241 GTTCACCCCTTTCTTGGAGCATACGATCAACCTGTAAGGAGATGGAAGACTTTGAGAGGAA 300  
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Db 301 ATGGGGAATGATCTTCCAGGAGTTCTGCTGTAAAGCGATCCCTCACCATTAACAAGATAA 360  
QY 361 GCAGAAATCTCCAGGCACTCTCTGTAAAGCGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420  
Db 361 GCAGAAATCTCCAGGCACTCTCTGTAAAGCGGCTGGCGTAGTGTGGCTTGGTCAAGGAA 420  
QY 421 CAGACAGGGCTGCACAAATGGCTCAGCTTCACTCCCAATCTTATTTCTGGGATTTACA 480  
Db 421 CAGACAGGGCTGCACAAATGGCTCAGCTTCACTCCCAATCTTATTTCTGGGATTTACA 480  
QY 481 CTCCTACAGTGTACAATGTCTCAGGGTATGGTCCAAACCAAGGCGCCAGAAAGGA 540  
Db 481 CTCCTACAGTGTACAATGTCTCAGGGTATGGTCCAAACCAAGGCGCCAGAAAGGA 540  
QY 541 GACATCATACTGGGAGGCTCTTCTCCCAATACACTTTGGAGTAGCGCCCAAGGATCAGGAC 600  
Db 541 GACATCATACTGGGAGGCTCTTCTCCCAATACACTTTGGAGTAGCGCCCAAGGATCAGGAC 600  
QY 601 TTAATAATCAGACCGGAGCGCAAAATGTATTCGGTACAAATTTTCGAGGCTTCGGATGG 660  
Db 601 TTAATAATCAGACCGGAGCGCAAAATGTATTCGGTACAAATTTTCGAGGCTTCGGATGG 660  
QY 661 CTCAGGGGATGATATTTCGCAATTGAAGAGATTAAACAAGTATGACTTTCTGCCCCAAT 720  
Db 661 CTCAGGGGATGATATTTCGCAATTGAAGAGATTAAACAAGTATGACTTTCTGCCCCAAT 720  
QY 721 ATCAACCTGGGATATGGCAATTTGACAGCTGTAAACCGTGTCCAGGCGCTAGAGCA 780  
Db 721 ATCAACCTGGGATATGGCAATTTGACAGCTGTAAACCGTGTCCAGGCGCTAGAGCA 780  
QY 781 ACACCTCAGCTTTGTGGCCAGAACAAATTCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840  
Db 781 ACACCTCAGCTTTGTGGCCAGAACAAATTCGACTCGCTGAACTTAGATGAGTTCTGTAAAC 840  
QY 841 TGCTGTGACCATATCCCAATCCCAATAGCAGTGGTGGGGCAACCGGTCAGGAATCTCC 900  
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QY 901 AGGGCTGTGGCCAAATCTATTTGGATTTATTTTACATTCACAGGTCAGCTATGCTCTCC 960  
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QY 961 AGCAGGCTCTCAGCAACAAGATGAGTACAAAGGCTTCTTGGAGCAACATCCCAATGAT 1020  
Db 961 AGCAGGCTCTCAGCAACAAGATGAGTACAAAGGCTTCTTGGAGCAACATCCCAATGAT 1020  
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Db 1081 ACCCTGGCAGCGACGATGACTATGGCCCGCCAGGCAATGACAAGTTCCGGGAGGAGGCC 1140  
QY 1141 GTTAAGAGGGAATCTGTATTGACTTCACTAGTAGATGATCTCTCAGTACTACACCCAGAAG 1200  
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QY 1201 CAGTTGGAGTTTCATCGCCAGCTGTATCCAGAACTCTCTGGCCCAAGTCTATCGTGTCTTC 1260  
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Db 1321 CGGATCTGGCTGGCAGCAGGCTTTGGGCGAGCTCTTCGCTCATTTGCCAAGCCAGATAC 1380

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Db 1381 TTCCACGTGTGGCGGCAACCATCGGCTTTCGCTCTCAGGGCGGGGCTATCCAGGGTTC 1440  
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Db 1681 CCCTACTGGAATATACACACCTGAGGATCTCTCAATGTATATGATACGTGGCCGCTTACTCC 1740  
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Db 1801 GGAATCTTGTGACATATTAATAAAGTTGAGGCTGGAGGCTCTCAACCATCTGTGTGAT 1860  
QY 1861 CTGAAGTTTACCAACAGCATGGGTGAGGAGTTGACTTTGACGATCAAGGTGAGCTCAAG 1920  
Db 1861 CTGAAGTTTACCAACAGCATGGGTGAGGAGTTGACTTTGACGATCAAGGTGAGCTCAAG 1920  
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Db 2341 ACCTCTTCTGCTGGGCTTTCATCAAGTTTCAGGAACATCCCATCTGTGAGGCGCAC 2400  
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[illegible]

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RESULT 2
US-09-687-477-17
; Sequence 17, Application US/09687477
; Patent No. 6463883
; GENERAL INFORMATION:
; APPLICANT: Aquabio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Becka, Marlies
; TITLE OF INVENTION: Methods for Raising P
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/09/687,477
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-09-687-477-17

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	Query Match	100.0%;	Score 4134;	DB 4;	Length 4134;	
	Best Local Similarity	100.0%;	Pred. NO. 0;			
	Matches 4134; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Dd	1 AATTCCGGTTCTGTCGGGTTCAGTCCCAAGTCTCCTCCAGTGCCAAATGAGAAAATCGTGTC	60				
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Qy	61 GCCATTACAGGAACAATGCATCATCTGTGTTTAATGAATAATTGTCAAGTATCTGAAGGT	120				

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Db	2461	ATCTTCATCGGAGAGCCAGGAGACTGSA	CTGTGCGCTCGGCCAACCGGCTTTGSCATC	2520
Qy	2521	AGCTTCGTCTGTGCATCTCTGCATCTCTG	TGAAGACCAACCGGCTGTCTGTGCTTC	2580
Db	2521	AGCTTCGTCTGTGCATCTCTGCATCTCTG	TGAAGACCAACCGGCTGTCTGTGCTTC	2580
Qy	2581	GAGGCCAAGATCCCAACCAAGCCTTCCAC	CGGCAAGTGGTGGGCTCAACCTGAGTTCTCTC	2640
Db	2581	GAGGCCAAGATCCCAACCAAGCCTTCCAC	CGGCAAGTGGGCTCAACCTGAGTTCTCTC	2640
Qy	2641	CTGGTCTTCTGTGCATCTCTGCTGCAAT	CGTCACTGCATCATCTGGCTCTACACCGCG	2700
Db	2641	CTGGTCTTCTGTGCATCTCTGCTGCAAT	CGTCACTGCATCATCTGGCTCTACACCGCG	2700
Qy	2701	CTCTCCCTCCAGCTACAGGAACCATGAGCT	GAGGACGAGGTCACTTTCATCACTCGGAC	2760
Db	2701	CTCTCCCTCCAGCTACAGGAACCATGAGCT	GAGGACGAGGTCACTTTCATCACTCGGAC	2760
Qy	2761	GAGGCTCGCTCATGCGCTTGGCTTCTCAT	CTGGGTACACCTGCATCATCTGGCTCTCGCGCGCATC	2820
Db	2761	GAGGCTCGCTCATGCGCTTGGCTTCTCAT	CTGGGTACACCTGCATCATCTGGCTCTCGCGCGCATC	2820
Qy	2821	TGCTTCTTCTTCCGCTTCAAGTCCCGT	TAGCTCCGGAACCTTCAACGAGGCTAAGTTC	2880
Db	2821	TGCTTCTTCTTCCGCTTCAAGTCCCGT	TAGCTCCGGAACCTTCAACGAGGCTAAGTTC	2880
Qy	2881	ATCACTTCAGCANGTGTATCTTCTTCAT	CTGATCTCTTTCATCCCGGCTATGTC	2940
Db	2881	ATCACTTCAGCANGTGTATCTTCTTCAT	CTGATCTCTTTCATCCCGGCTATGTC	2940
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Qy	3061	AACACCATCAGAGAGTGCGCTCGACGAC	CGCGCGCCACCGCTTCAAGTGGCGGCGCG	3120
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Qy	3121	GCACCCCTCGCGCGCAGCGCGCTCTCG	CAAGCGTCCAGCAGACCTGTGCGGCTCCACC	3180
Db	3121	GCACCCCTCGCGCGCAGCGCGCTCTCG	CAAGCGTCCAGCAGACCTGTGCGGCTCCACC	3180
Qy	3181	ATCTCTCGCCCGCTGTCTCACTCTCGCG	CGCGGCTCAACATGAGATGACAGCGCTGC	3240
Db	3181	ATCTCTCGCCCGCTGTCTCACTCTCGCG	CGCGGCTCAACATGAGATGACAGCGCTGC	3240
Qy	3241	AGCAGCAGAAGTTCAGCTTTCGCGAGCG	GACCGTCAACCTGTCTGCTCAGTTTCGAGGAG	3300
Db	3241	AGCAGCAGAAGTTCAGCTTTCGCGAGCG	GACCGTCAACCTGTCTGCTCAGTTTCGAGGAG	3300
Qy	3301	ACAGGCGGATACGCCACCTTCAGCCGCA	CGCGCCGACGACGAGAACTCGGCGGATGCGCGC	3360
Db	3301	ACAGGCGGATACGCCACCTTCAGCCGCA	CGCGCCGACGACGAGAACTCGGCGGATGCGCGC	3360
Qy	3361	AGCGGCGACACTGCGCATCTAGACAC	CCAGCACCGGCGCGCTCAGAAATCCGAGCCCC	3420
Db	3361	AGCGGCGACACTGCGCATCTAGACAC	CCAGCACCGGCGCGCTCAGAAATCCGAGCCCC	3420
Qy	3421	CAGCCCGCCAACGATGCCGATACAGAG	CGCGCGCACCAAGGCGACCTTAGAGTGC	3480
Db	3421	CAGCCCGCCAACGATGCCGATACAGAG	CGCGCGCACCAAGGCGACCTTAGAGTGC	3480
Qy	3481	GGCGGCGACGAGGCGCCCCCAACTAT	TGGAGGAACCTTAATCCTCTCCATCAAC	3540
Db	3481	GGCGGCGACGAGGCGCCCCCAACTAT	TGGAGGAACCTTAATCCTCTCCATCAAC	3540
Qy	3541	CCCAAGAACATCTTCACGGCAGCACCG	TGCACAACTGACATCAACTCTTAACCGGTGGC	3600

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QY 601 TTAAATTCAGACCGGAGCGACAAATGTTATTCGGTACAAATTTTCGAGGCTTCGGATGG 660  
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US-09-687-476-17

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Query Match      100.0%; Score 4134; DB 4; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134: Conservative 0; Mismatches 0; Indels 0;
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CS-05-687-7478-17									
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Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	AATTCGGTTGCTGTGGTTTCAGTCCAAAGTCTCCTCCAGTGCAGAAATGAGAAATCGTGTGC	60						
QY	61	GCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATGTCAGTTATCTGAAGGT	120						
DB	61	GCATTACAGGAACATGCACTACATCTGTGTTAATGAAATATGTCAGTTATCTGAAGGT	120						
QY	121	TATTAAATGTTTCTGCAGGATGCTTCACAGAGAAATCAATTCGCAGCTTTTCCCAAT	180						
DB	121	TATTAAATGTTTCTGCAGGATGCTTCACAGAGAAATCAATTCGCAGCTTTTCCCAAT	180						
QY	181	GTCAATTGTATGAATTAACCTGACCAAAAGGATGTAAACAAATGGAACAAAGCTGAGGACC	240						
DB	181	GTCAATTGTATGAATTAACCTGACCAAAAGGATGTAAACAAATGGAACAAAGCTGAGGACC	240						
QY	241	GTTCAACCTTTCTTGGAGATACGATCAACCTGAAAGGATGGAAGATGGAAGATGGAAGAA	300						
DB	241	GTTCAACCTTTCTTGGAGATACGATCAACCTGAAAGGATGGAAGATGGAAGATGGAAGAA	300						
QY	301	ATGGGATTTGATCTTCCAGGAGTCTGTGTTAAAGCGATCCCTCACCAATTACAAAGATAA	360						
DB	301	ATGGGATTTGATCTTCCAGGAGTCTGTGTTAAAGCGATCCCTCACCAATTACAAAGATAA	360						
QY	361	GCAGAAATCCTCAGGCATCTCTGTAAACGGGCTGGCGTAGTGTGGTTCAGAGAA	420						
DB	361	GCAGAAATCCTCAGGCATCTCTGTAAACGGGCTGGCGTAGTGTGGTTCAGAGAA	420						
QY	421	CAGAGACAGGGCTGCACAATGGCTCAGCTTCACTGSCAACTCTTAATCTTGGGATTTACA	480						
DB	421	CAGAGACAGGGCTGCACAATGGCTCAGCTTCACTGSCAACTCTTAATCTTGGGATTTACA	480						
QY	481	CTCTCAGTCGTACAATGTCTCAGGGTATGGTCCAAACCAAGGGCCGAGAGAAAGGA	540						
DB	481	CTCTCAGTCGTACAATGTCTCAGGGTATGGTCCAAACCAAGGGCCGAGAGAAAGGA	540						
QY	541	GACATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCGCCCAAGGATCAGGAC	600						
DB	541	GACATCATACTGGGAGGTCTCTTCCCAATACACTTTGGAGTAGCGCCCAAGGATCAGGAC	600						
QY	601	TTAAATCGAGACCGGAGCGCAAAATGTATTCGGTACAATTTTCAGGCTTCCGATGG	660						
DB	601	TTAAATCGAGACCGGAGCGCAAAATGTATTCGGTACAATTTTCAGGCTTCCGATGG	660						
QY	661	CTCCAGGCGATGATTTGCAATTCAGAGATTAAACAGTATGACTTTTCCTGCCCAAT	720						
DB	661	CTCCAGGCGATGATTTGCAATTCAGAGATTAAACAGTATGACTTTTCCTGCCCAAT	720						
QY	721	ATCACCTGGGATATCGCATATTTGACACGTGTAAACCGGTGTCGAAGGCGCTAGAGGCA	780						
DB	721	ATCACCTGGGATATCGCATATTTGACACGTGTAAACCGGTGTCGAAGGCGCTAGAGGCA	780						
QY	781	ACACTCAGCTTTGCGCCAGAACAAATCGACTCGCTGACTTAGATGATGTTCTGTAAC	840						
DB	781	ACACTCAGCTTTGCGCCAGAACAAATCGACTCGCTGACTTAGATGATGTTCTGTAAC	840						
QY	841	TGCTCTGACCATATCCCATTCACATAGCAGTGGTTCGGGCAACCGGGTCAGGAATCTCC	900						
DB	841	TGCTCTGACCATATCCCATTCACATAGCAGTGGTTCGGGCAACCGGGTCAGGAATCTCC	900						
QY	901	ACGGCTGTGGCAATCTATTGGGATTTTACATTCACAGGTCAGCTATGCTCTCTCG	960						
DB	901	ACGGCTGTGGCAATCTATTGGGATTTTACATTCACAGGTCAGCTATGCTCTCTCTCG	960						
QY	961	AGCAGGCTGCTCAGCAACAAAGATGAGTACAAGGCTTCTTGGAGGACCATCCCCAATGAT	1020						
DB	961	AGCAGGCTGCTCAGCAACAAAGATGAGTACAAGGCTTCTTGGAGGACCATCCCCAATGAT	1020						
QY	1021	GAGCAACAGGCCACCGCCCATCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080						
DB	1021	GAGCAACAGGCCACCGCCCATCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080						
QY	1081	ACCCTGGCAGCGAGCATGACTATGGCCGCCACGCAATTGACAAAGTTCCGGGAGAGGCC	1140						
DB	1081	ACCCTGGCAGCGAGCATGACTATGGCCGCCACGCAATTGACAAAGTTCCGGGAGAGGCC	1140						
QY	1141	GTTAAGAGGGACATCTGTATTGACTTTCAGTGGAGATGATCTCTCAGTACTACACCCAGAAG	1200						
DB	1141	GTTAAGAGGGACATCTGTATTGACTTTCAGTGGAGATGATCTCTCAGTACTACACCCAGAAG	1200						
QY	1201	CAGTTTGGAGTTTCATCGCCGAGCTCATCCAGAACTCTTCGGCCAAAGGTCATCGTGGTCTTC	1260						
DB	1201	CAGTTTGGAGTTTCATCGCCGAGCTCATCCAGAACTCTTCGGCCAAAGGTCATCGTGGTCTTC	1260						
QY	1261	TCCAAATGCCCCGACCTCGAGCCGCTCATTCAGAGATAGTTCGGAGAAACATCACCCGAT	1320						
DB	1261	TCCAAATGCCCCGACCTCGAGCCGCTCATTCAGAGATAGTTCGGAGAAACATCACCCGAT	1320						
QY	1321	CGGATCTCGCTGGCCAGCGAGCTTTGGCCAGACTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380						
DB	1321	CGGATCTCGCTGGCCAGCGAGCTTTGGCCAGACTCTTCGCTCATTTGCCAAGCCAGAGTAC	1380						
QY	1381	TTTCCACGTGGTCCGGGCCACCATCGGCTTGCTCTCAGGGCGGGCGTATTCACAGGGTTC	1440						
DB	1381	TTTCCACGTGGTCCGGGCCACCATCGGCTTGCTCTCAGGGCGGGCGTATTCACAGGGTTC	1440						
QY	1441	PACRAAGTTCTGTGAGGAGTCCACCCAGCAGAGGTCCTCGACAAATGGGTTGTCAAGGAG	1500						
DB	1441	PACRAAGTTCTGTGAGGAGTCCACCCAGCAGAGGTCCTCGACAAATGGGTTGTCAAGGAG	1500						
QY	1501	TTTCTGGGAGGAGACCTTCAACTGCTACTCTCAACGAGAAAGCCCTGACGCACTGAAAGAT	1560						
DB	1501	TTTCTGGGAGGAGACCTTCAACTGCTACTCTCAACGAGAAAGCCCTGACGCACTGAAAGAT	1560						
QY	1561	TCCAGGTGCCCCCTGCACGAGACCGCGGCTCAAGGGACGGCTTCAAGGCGGGGAACTCC	1620						
DB	1561	TCCAGGTGCCCCCTGCACGAGACCGCGGCTCAAGGGACGGCTTCAAGGCGGGGAACTCC	1620						
QY	1621	AGACGCAAGCCCTACGCCACCCCTGCACCTGGGAGGAGAAACATCACACGCTGGAGACC	1680						
DB	1621	AGACGCAAGCCCTACGCCACCCCTGCACCTGGGAGGAGAAACATCACACGCTGGAGACC	1680						
QY	1681	CCCTACCTGGATATACACCTGAGGATCTCTCAATGATATACGTGGCGCTCTACTCC	1740						
DB	1681	CCCTACCTGGATATACACCTGAGGATCTCTCAATGATATACGTGGCGCTCTACTCC	1740						
QY	1741	ATTGCTCAGCCCTGCAAGACATCCACTCTTGAAACCCGCGACGGGCATCTTTGCAAAAC	1800						
DB	1741	ATTGCTCAGCCCTGCAAGACATCCACTCTTGCAAAACCCGCGACGGGCATCTTTGCAAAAC	1800						
QY	1801	GGATCTTGTGAGATATATAAAGTTGAGGCTTGAGGCTTGAGGCTCTCAACATCTGCTGCAT	1860						
DB	1801	GGATCTTGTGAGATATATAAAGTTGAGGCTTGAGGCTTGAGGCTCTCAACATCTGCTGCAT	1860						
QY	1861	CTGAAGTTTACCAAC							

[illegible]

; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous  
; FILE OF INVENTION: Fish

; CURRENT APPLICATION NUMBER: US/09/687,372

; CURRENT FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 4134

; TYPE: DNA

; ORGANISM: Dogfish Shark

US-09-687-372-17

Query Match 100.0%; Score 4134; DB 4; Length 4134;  
Best Local Similarity 100.0%; Pred No. 0;  
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTCGGTTGCTGCGTTTCAGTCCAAAGTCTCTCCAGTGCAAAATGAGAAATGTTGTC 60  
Db 1 AATTCGGTTGCTGCGTTTCAGTCCAAAGTCTCTCCAGTGCAAAATGAGAAATGTTGTC 60  
Qy 61 GCCATTACAGGACATGCACTACATCTGTTTAATGAATATTTGTCAGTTATCTGAAGT 120  
Db 61 GCCATTACAGGACATGCACTACATCTGTTTAATGAATATTTGTCAGTTATCTGAAGT 120  
Qy 121 TATTAATAATGTTTCTGCAAGGATGGCTTCCAGAGAAATCAATCTGCGAGTTTCCCAT 180  
Db 121 TATTAATAATGTTTCTGCAAGGATGGCTTCCAGAGAAATCAATCTGCGAGTTTCCCAT 180  
Qy 181 GTCAATTGATGAATACTACCAAGAGGATGTAAACAAATGGAACAAAGCTGAGACAC 240  
Db 181 GTCAATTGATGAATACTACCAAGAGGATGTAAACAAATGGAACAAAGCTGAGACAC 240  
Qy 241 GTTCAACCTTTCTTGAGAGATAGATCAACCTGGAAGGATGGAAGATTTGAGAGGAA 300  
Db 241 GTTCAACCTTTCTTGAGAGATAGATCAACCTGGAAGGATGGAAGATTTGAGAGGAA 300  
Qy 301 ATGGGATGATGTTTCCAGGATTCGTGTAAAGGATTCCTCAACCAATTAACAAAGATA 360  
Db 301 ATGGGATGATGTTTCCAGGATTCGTGTAAAGGATTCCTCAACCAATTAACAAAGATA 360  
Qy 361 GCAGAAATCCTCCAGGATCCTCTGTAAACGGGCTGGGCTAGTGGTTCAGGAA 420  
Db 361 GCAGAAATCCTCCAGGATCCTCTGTAAACGGGCTGGGCTAGTGGTTCAGGAA 420  
Qy 421 CAGAGACAGGCTGCAATAGGCTCAGCTTCACTGCCAACTTATTTCTGGGATTTACA 480  
Db 421 CAGAGACAGGCTGCAATAGGCTCAGCTTCACTGCCAACTTATTTCTGGGATTTACA 480  
Qy 481 CTCCTACAGTCTGATGATGTTCTCAGGATGTTCTCAACCAAGGCTGAGGATGAGGA 540  
Db 481 CTCCTACAGTCTGATGATGTTCTCAGGATGTTCTCAACCAAGGCTGAGGATGAGGA 540  
Qy 541 GACATCATAGTGGAGGCTCTTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600  
Db 541 GACATCATAGTGGAGGCTCTTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600  
Qy 601 TTAATAATCAGACCGAGGCGCAAAATGATATTCGGTCAATTTTCAGAGGCTTCGATGG 660  
Db 601 TTAATAATCAGACCGAGGCGCAAAATGATATTCGGTCAATTTTCAGAGGCTTCGATGG 660  
Qy 661 CTCAGGCGATGATATTCGCAATTCAGAGATTAACAAAGTATGACATGACATTTCTGCCCAAT 720  
Db 661 CTCAGGCGATGATATTCGCAATTCAGAGATTAACAAAGTATGACATGACATTTCTGCCCAAT 720  
Qy 721 ATCAACCTCGGATATGCGATATTTGACACGTTAAACCGCTGTCACAGGCGCTAGAGCA 780  
Db 721 ATCAACCTCGGATATGCGATATTTGACACGTTAAACCGCTGTCACAGGCGCTAGAGCA 780  
Qy 781 ACACCTCAGCTTTGTCGCGCAGACAAATTCGATCGCTGACATGATGATGATGATGATG 840  
Db 781 ACACCTCAGCTTTGTCGCGCAGACAAATTCGATCGCTGACATGATGATGATGATGATG 840

Qy 841 TGCTCTGACCATATCCCATCCACATAGCAGTGGTGGGGCAACCGGGTCAGGAATCTCC 900  
Db 841 TGCTCTGACCATATCCCATCCACATAGCAGTGGTGGGGCAACCGGGTCAGGAATCTCC 900  
Qy 901 ACAGCTGTGGCCCAATCTATTGGGATTTATTATTCACAGGCTCAGCTATGCTCTCTCG 960  
Db 901 ACAGCTGTGGCCCAATCTATTGGGATTTATTATTCACAGGCTCAGCTATGCTCTCTCG 960  
Qy 961 AGCAGGCTGCTCAGCAACAAGATGATGATCAAGGCTTCTCAGGACCATCCCAATGAT 1020  
Db 961 AGCAGGCTGCTCAGCAACAAGATGATGATCAAGGCTTCTCAGGACCATCCCAATGAT 1020  
Qy 1021 GAGCAACAGGCGCACGGCCATGGCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080  
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Qy 1081 ACCCTGAGCGCAGACGATGATGAGGCGCCAGGCAATTGACAAAGTTCGCGAGGAGGCC 1140  
Db 1081 ACCCTGAGCGCAGACGATGATGAGGCGCCAGGCAATTGACAAAGTTCGCGAGGAGGCC 1140  
Qy 1141 GTTAAGAGGACATCTGTTATTTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200  
Db 1141 GTTAAGAGGACATCTGTTATTTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG 1200  
Qy 1201 CAGTTGAGTTTCATCGCCGACGTCATCCAGAACTCTCTCGGCCAAGGTCATCGTGTCTTC 1260  
Db 1201 CAGTTGAGTTTCATCGCCGACGTCATCCAGAACTCTCTCGGCCAAGGTCATCGTGTCTTC 1260  
Qy 1261 TCCAAATGGCCCGACCTGGAGCGGCTCATCCAGAGATAGTTCCGAGAAACATCAACCGAT 1320  
Db 1261 TCCAAATGGCCCGACCTGGAGCGGCTCATCCAGAGATAGTTCCGAGAAACATCAACCGAT 1320  
Qy 1321 CGGATCTGGCTGGCGAGCGGCTTGGGCGAGCTCTTCGCTCATTTCCCAAGCCAGAGTAC 1380  
Db 1321 CGGATCTGGCTGGCGAGCGGCTTGGGCGAGCTCTTCGCTCATTTCCCAAGCCAGAGTAC 1380  
Qy 1381 TTCCACGCTGGTGGCGGCGACCATCGGCTTCCGCTCATCGGCGGGGCTATCCAGAGGTT 1440  
Db 1381 TTCCACGCTGGTGGCGGCGACCATCGGCTTCCGCTCATCGGCGGGGCTATCCAGAGGTT 1440  
Qy 1441 AACAGTTCTGAGAGAGGTCACCCAGCAGGCTCTCGCAAAATGGGTTTGTCAAGGAG 1500  
Db 1441 AACAGTTCTGAGAGAGGTCACCCAGCAGGCTCTCGCAAAATGGGTTTGTCAAGGAG 1500  
Qy 1501 TTTGGAGGAGACCTTTCAATCTGCTACTTCCAGAGAACCTCTGACGAGCTGGAAGAAT 1560  
Db 1501 TTTGGAGGAGACCTTTCAATCTGCTACTTCCAGAGAACCTCTGACGAGCTGGAAGAAT 1560  
Qy 1561 TCCAAATGGCCCGACCTGGAGCGGCTCAGGCGGAGGCTCCCAAGCGGGGACTCC 1620  
Db 1561 TCCAAATGGCCCGACCTGGAGCGGCTCAGGCGGAGGCTCCCAAGCGGGGACTCC 1620  
Qy 1621 AGACGACAGCCCTAGCCCAACCTCTGACCTGGGGAGGAGAACATCACACGCTGGAGACC 1680  
Db 1621 AGACGACAGCCCTAGCCCAACCTCTGACCTGGGGAGGAGAACATCACACGCTGGAGACC 1680  
Qy 1681 CCCTACCTGATATATACACCTGAGGATCTCTCAATGATATGATGCTGGCGCTCTACTCC 1740  
Db 1681 CCCTACCTGATATATACACCTGAGGATCTCTCAATGATATGATGCTGGCGCTCTACTCC 1740  
Qy 1741 ATTGCTCACGCCCTGAGAGCATCCACTTTGCAAAACCGGACCGGCACTTTTGCAAAAC 1800  
Db 1741 ATTGCTCACGCCCTGAGAGCATCCACTTTGCAAAACCGGACCGGCACTTTTGCAAAAC 1800  
Qy 1801 GGATCTTTGTCAGATATTAATAAAGTTGAGGCTGCGAGTCTCTCAACCATCTGTGTCAT 1860  
Db 1801 GGATCTTTGTCAGATATTAATAAAGTTGAGGCTGCGAGTCTCTCAACCATCTGTGTCAT 1860  
Qy 1861 CTCAGTTTACCAACAGCATGGGTGAGGCTGAGGCTGAGGCTCTGAGGCTCAAGTCAAG 1920  
Db 1861 CTCAGTTTACCAACAGCATGGGTGAGGCTGAGGCTGAGGCTCTGAGGCTCAAGTCAAG 1920

Qy	1921	GGGAAC	TACACCA	TATCA	ACTGCG	AGCTCT	CCG	CAGAG	GATGA	ATCG	GTGTT	GTTC	CAAT	1988
Db	1921	GGGAAC	TACACCA	TATCA	ACTGCG	AGCTCT	CCG	CAGAG	GATGA	ATCG	GTGTT	GTTC	CAAT	1988
Qy	1981	GAGTGG	CGCAACT	ACAA	CGCCTA	AGCCAGT	CA	CCAGT	CA	CCAGT	CA	CAACAT	CAACGAA	2040
Db	1981	GAGTGG	CGCAACT	ACAA	CGCCTA	AGCCAGT	CA	CCAGT	CA	CCAGT	CA	CAACAT	CAACGAA	2040
Qy	2041	AAAA	TCTCTG	AGTGTG	CTTCT	CAAA	AGTGG	TTCT	CTTT	CTT	CTT	CTT	CTT	2100
Db	2041	AAAA	TCTCTG	AGTGTG	CTTCT	CAAA	AGTGG	TTCT	CTTT	CTT	CTT	CTT	CTT	2100
Qy	2101	GTGCGG	GCAC	CCAGAA	GGGAT	CAT	CG	AGGGG	GAGCC	ACCT	GTGCT	TTTGA	TGCATG	2160
Db	2101	GTGCGG	GCAC	CCAGAA	GGGAT	CAT	CG	AGGGG	GAGCC	ACCT	GTGCT	TTTGA	TGCATG	2160
Qy	2161	GCATG	TCAG	AGGAG	AGTT	CAGT	GT	GA	AAAA	CGAT	CA	AGT	CGTGT	2220
Db	2161	GCATG	TCAG	AGGAG	AGTT	CAGT	GT	GA	AAAA	CGAT	CA	AGT	CGTGT	2220
Qy	2221	AATGAT	TTCTG	GTG	CGAAT	GAGAAC	CA	CAGCT	CGT	GCAT	CGC	CA	AGGAGAT	2280
Db	2221	AATGAT	TTCTG	GTG	CGAAT	GAGAAC	CA	CAGCT	CGT	GCAT	CGC	CA	AGGAGAT	2280
Qy	2281	TCGTG	GA	CGAG	CCCTT	CGGAT	CGCT	CT	GACCA	CTT	TCG	CGT	ACTTGG	2340
Db	2281	TCGTG	GA	CGAG	CCCTT	CGGAT	CGCT	CT	GACCA	CTT	TCG	CGT	ACTTGG	2340
Qy	2341	ACCTC	CTT	CTG	CTGGG	CTT	CT	CA	AGTT	TCAG	GAACA	CT	CCCAT	2400
Db	2341	ACCTC	CTT	CTG	CTGGG	CTT	CT	CA	AGTT	TCAG	GAACA	CT	CCCAT	2400
Qy	2401	AACCG	GAGTTG	TCT	ACCT	GTGCT	CTT	CT	CCCT	CAT	CT	GCTG	TTCTCC	2460
Db	2401	AACCG	GAGTTG	TCT	ACCT	GTGCT	CTT	CT	CCCT	CAT	CT	GCTG	TTCTCC	2460
Qy	2461	ATCTT	CA	TCG	CGAG	CCAGG	A	CTG	AC	CTGT	CGG	CT	CGC	2520
Db	2461	ATCTT	CA	TCG	CGAG	CCAGG	A	CTG	AC	CTGT	CGG	CT	CGC	2520
Qy	2521	AGCTT	CG	CTG	CTGCAT	CT	CTG	TC	AG	ACCA	CC	CGG	GTGCTG	2580
Db	2521	AGCTT	CG	CTG	CTGCAT	CT	CTG	TC	AG	ACCA	CC	CGG	GTGCTG	2580
Qy	2581	GAGGC	CAAG	ATCCC	AC	CAG	CT	CC	AC	CGA	AGTGG	GTG	GTCT	2640
Db	2581	GAGGC	CAAG	ATCCC	AC	CAG	CT	CC	AC	CGA	AGTGG	GTG	GTCT	2640
Qy	2641	CTG	GTCTT	CTCT	CGAT	CT	CGT	CA	CT	CGAT	CT	CGT	CA	2700
Db	2641	CTG	GTCTT	CTCT	CGAT	CT	CGT	CA	CT	CGAT	CT	CGT	CA	2700
Qy	2701	CCTC	CT	CCAGT	ACAG	GA	CCAT	GAT	GAG	GA	CGAG	GT	CT	2760
Db	2701	CCTC	CT	CCAGT	ACAG	GA	CCAT	GAT	GAG	GA	CGAG	GT	CT	2760
Qy	2761	GAGG	GT	CTG	TCAT	GGG	CTT	CGT	CA	TCG	GGT	TC	TC	2820
Db	2761	GAGG	GT	CTG	TCAT	GGG	CTT	CGT	CA	TCG	GGT	TC	TC	2820
Qy	2821	TGCTT	CTT	CTT	CGC	CTT	CA	AGT	CCG	G	AG	AACT	TC	2880
Db	2821	TGCTT	CTT	CTT	CGC	CTT	CA	AGT	CCG	G	AG	AACT	TC	2880
Qy	2881	ATC	ACCTT	CAG	CA	TGTT	GAT	CTT	CT	CA	TG	TCG	AT	2940
Db	2881	ATC	ACCTT	CAG	CA	TGTT	GAT	CTT	CT	CA	TG	TCG	AT	2940
Qy	2941	AGC	AC	TAC	GC	CA	AGT	TTG	TC	GG	CGT	GG	AGT	3000
Db	2941	AGC	AC	TAC	GC	CA	AGT	TTG	TC	GG	CGT	GG	AGT	3000
Qy	3001	GGG	GT	GTG	GGC	TG	CA	TTT	ACT					

[illegible]



Db 4081 AAGCGCCGACAGCAACGG 4134

RESULT 5

US-09-975-553-17

; Sequence 17, Application US/09975553

; Patent No. 6564747

; GENERAL INFORMATION:

; APPLICANT: Hatriis, H. William, Jr.

; APPLICANT: Russell, David R.

; APPLICANT: Nearing, Jacqueline

; APPLICANT: Betka, Marlies

; TITLE OF INVENTION: Fish

; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous

; FILE REFERENCE: 2213.1004-001

; CURRENT APPLICATION NUMBER: US/09/975,553

; CURRENT FILING DATE: 2001-10-11

; PRIOR APPLICATION NUMBER: 09/687,477

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: 09/687,476

; PRIOR FILING DATE: 2000-10-12

; PRIOR APPLICATION NUMBER: 09/687,372

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 4134

; TYPE: DNA

; ORGANISM: Dogfish Shark

US-09-975-553-17

Query Match 100.0%; Score 4134; DB 4; Length 4134;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGGTGTCTGCGTTCAGTCCAAAGTCTCTCCAGTGCAGAAATGAGAAATGCTGTC 60

DB 1 AATTCGGTGTCTGCGTTCAGTCCAAAGTCTCTCCAGTGCAGAAATGAGAAATGCTGTC 60

QY 61 GCATTACAGGAACATGCACTACATCTGTGTTAAATGAAATATGTGAGTATCTGAAAGT 120

DB 61 GCATTACAGGAACATGCACTACATCTGTGTTAAATGAAATATGTGAGTATCTGAAAGT 120

QY 121 TATTAATGTTTCTGCAAGATGGCTTCCAGAGAAATCAATTCGACGTTTCCCAT 180

DB 121 TATTAATGTTTCTGCAAGATGGCTTCCAGAGAAATCAATTCGACGTTTCCCAT 180

QY 181 GTCAATTGATGAATACTGACCAAAAGGATGTAAACAAAATGGAACAAAGCTGAGGACCAC 240

DB 181 GTCAATTGATGAATACTGACCAAAAGGATGTAAACAAAATGGAACAAAGCTGAGGACCAC 240

QY 241 GTTCAACCTTCTTGGAGATACGATCAACCTGAGGAGATGGAAGCTTGGAGGAA 300

DB 241 GTTCAACCTTCTTGGAGATACGATCAACCTGAGGAGATGGAAGCTTGGAGGAA 300

QY 301 ATGGGATTTGATCTTCCAGAGTTCGTCTGTTAAAGCGATCCCTCAACATTAACAAAGATAA 360

DB 301 ATGGGATTTGATCTTCCAGAGTTCGTCTGTTAAAGCGATCCCTCAACATTAACAAAGATAA 360

QY 361 GCAGAAATCTCCAGGATCTCTGTAAACGGGCTGGCGTAGTGTGGTGGTCAAGGAA 420

DB 361 GCAGAAATCTCCAGGATCTCTGTAAACGGGCTGGCGTAGTGTGGTGGTCAAGGAA 420

QY 421 CAGAGACAGGCTGCAATGCTCAGCTTCACTGCAACTCTTATTTCTGGGATTTTACA 480

DB 421 CAGAGACAGGCTGCAATGCTCAGCTTCACTGCAACTCTTATTTCTGGGATTTTACA 480

QY 481 CTCCTACAGTCGTAATGCTCAGGGTATGTGCAAAACCAAGGGCCGAGAAAGGA 540

DB 481 CTCCTACAGTCGTAATGCTCAGGGTATGTGCAAAACCAAGGGCCGAGAAAGGA 540

QY 541 GACATCACTGGGAGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600

Db 541 GACATCACTGGGAGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600

QY 601 TTAATAATCGAGACCGGAGGCGACAAAATGTTATTCGGTACAAATTTTCGAGGCTTCCGATGG 660

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DB 841 TGCTTGACCATATCCCATCCAAATAGCAGTGGTGGGCGCAACCGGTCAGGAACTCC 900

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DB 901 ACGGCTGTGGCAATCTATTGGGATTTATTTTACATTTCCACAGGTCAGCTATGCTCTCTCG 960

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DB 1021 GAGCAACAGCGCCAGGCGCATGCGCGGAGATCATCGAGCACTTCCAGTGGAACTCGGTGGGA 1080

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DB 1621 AGACGAGACGCTTCAGCGGAGGAGGAGAAACATTCAGCGAGCTGAAGAAT 1680



1681 CCTACCTGGATATATACACACTGAGGATCTCCTACAATGTATATACGTGGCGGTCTACTCC 1740  
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1801 GGATCTTGTGCAGATATTAATAAAGTTGAGGCTTGGCAGGTCCTCAACCATCTGCTGCAT 1860  
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1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTGTGACTTTGACGATCAAGGTGACCTCAAG 1920  
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1921 GGGAACTACACCATTAATCAACTGGGAGCTCTCCGACAGGATGAATCGGTGTGTTCCAT 1980  
1981 GAGGTGGGCAACTACAAACGCTTACGCTAAGCCCAAGTACCGACTCAACATCAACGAAAAG 2040  
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2101 GTCCGGGACACAGGAAGGGATCATCGAGGGGAGCCACCTGCTGTTTGAATGCATG 2160  
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2161 GCATGTGAGAGGAGTTCAGTATGAAACGATGCAAGTGCCTGTACAAAGTGCCCG 2220  
2161 GCATGTGAGAGGAGTTCAGTATGAAACGATGCAAGTGCCTGTACAAAGTGCCCG 2220  
2221 AATGATTTCTGTCGAATGAGAACACACAGCTCGTGCATCGCCCAAGGAGATCGAGTACCTG 2280  
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2341 ACCTCTTCTGCTGGGTCTTTCATCAAGTTTCAGAAACATCCCATCTGTAAGGCCACC 2400  
2341 ACCTCTTCTGCTGGGTCTTTCATCAAGTTTCAGAAACATCCCATCTGTAAGGCCACC 2400  
2401 AACCGGAGTTTCTTACCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460  
2401 AACCGGAGTTTCTTACCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTCGCTC 2460  
2461 ATCTTCATCGGAGCCGAGGACTGGACCTGCTCGCTCCGCGCAACCGGCTTTGGCATC 2520  
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2701 CTTCCCTCAGTACAGGAACCAATGAGTGGAGGACGAGGTCTTTCATCACTGAGTGCAC 2760  
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Qy      3961  TTGCAACAGGAATATAATGACTGTAAACAAAAAATTTGTTATTTCTTAAAAATGCAAA 4020
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Qy      4081  AAAAAAATGTAATAATTTGGTAAATTTCTGTACATTAATGCAATTTCTTGATA 4134
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## RESULT 6

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US-10-270-795-17
; Sequence 17, Application US/10270795
; Patent No. 6637371
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.2002-000
; CURRENT APPLICATION NUMBER: US/10/270,795
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,372
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-795-17
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Query Match      100.0%; Score 4134; DB 4; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      181  GTCATTGTATGAATACCTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGAC 240
Qy      241  GTTCACCTTTCTTGAGCATACGATCAACCTGAGGAGATGGAAGCTTGAAGGAA 300
Db      241  GTTCACCTTTCTTGAGCATACGATCAACCTGAGGAGATGGAAGCTTGAAGGAA 300
Qy      301  ATGGGATTTGATCTTCCAGGATTTCTGCTGTTAAAGCGATCCCTCACCATTACAAAGATA 360
Db      301  ATGGGATTTGATCTTCCAGGATTTCTGCTGTTAAAGCGATCCCTCACCATTACAAAGATA 360
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Db      421  CAGAGCAGGGCTGCACAAATGGCTCAGCTTCACTGCCAACTCTTATTTCTTGGATTTACA 480
Qy      481  CTCTCAGTCGTACAAATGTCTCAGGGTATGTTTCCAAACCAAGGCCCCAGAGAAGA 540
Db      481  CTCTCAGTCGTACAAATGTCTCAGGGTATGTTTCCAAACCAAGGCCCCAGAGAAGA 540
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Db      541  GACATCATCTGGAGGCTCTCTTCCCAATACACTTTGGAGTAGCCCGCAGGATCAGGAC 600
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RESULT 7
US-10-270-876-17
; Sequence 17, Application US/10270876
; Patent No. 665318
; GENERAL INFORMATION:
; APPLICANT: Aquabio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Neuring, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/10/270,876
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,477
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-876-17

Query Match 100.0%; Score 4134; DB 4; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 781 ACACCTCAGCTTTGTGCGCCAGAACAAAATCGACTCGCTGAACTTAGATGAGTCTGTAAAC 840
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DB 841 TGCTCTGACCATATCCATCCCAATAGCAGTGTGCGGCGCAACCGGCTCAGGAATCTCC 900
QY 901 ACGGCTGTGCGCAATCTATTGGGATTTATTACATTTCCACAGGTGAGTATGCTCTCG 960
DB 901 ACGGCTGTGCGCAATCTATTGGGATTTATTACATTTCCACAGGTGAGTATGCTCTCG 960
QY 961 AGCAGCTGCTCAGCAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 AGCAGCTGCTCAGCAACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 GAGCAACAGGCGCACGCGCATGCGCGGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGA 1080
DB 1021 GAGCAACAGGCGCACGCGCATGCGCGGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGA 1080
QY 1081 ACCCTGCGACCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 ACCCTGCGACCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 GTTAAAGAGGAGATCTGTATTGATTTTCACTGAGATGATCTCTCAGTACTACACCCAGAA 1200
DB 1141 GTTAAAGAGGAGATCTGTATTGATTTTCACTGAGATGATCTCTCAGTACTACACCCAGAA 1200
QY 1201 CAGTGTGAGTTCAATCGCGGAGCTGATCCAGAACTCTCGGCGCAAGGTGATCGTGTCTTC 1260
DB 1201 CAGTGTGAGTTCAATCGCGGAGCTGATCCAGAACTCTCGGCGCAAGGTGATCGTGTCTTC 1260

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1261 TCCTAATGCGCCCGAAGCTGAGAGCGGTCTCATTCAGGAGATAGTTGGAGAAAAATCACCGAT 1320  
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1321 CGGATCTGGCTGGCCAGAGAGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380  
1321 CGGATCTGGCTGGCCAGAGAGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTAC 1380  
1381 TTCCACGTTGCTGGCGGACCAATCGGCTTCGCTCTCAGGGGGGCGTATCCCAAGGTTTC 1440  
1381 TTCCACGTTGCTGGCGGACCAATCGGCTTCGCTCTCAGGGGGGCGTATCCCAAGGTTTC 1440  
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1441 AACAAATTCCTGAAGAGAGTCCACCCAGCAGAGTCTCTGGACAATGGGTTTGTCAAGGAG 1500  
1501 TTCTCGGAGGAGACCTTCAACTGCTACTTCAACCGAGAGAGACCTTCAACCGAGAGTCC 1560  
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1561 TCCAAAGTTCCTCGCAGCGGACCGGCTCAAGGGGAGCGGCTCCAAAGGCGGGAATCTCC 1620  
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1621 AGACGAGCAGCCTACGCGCACCCCTGCACTGGGAGAGAGAACATCACAGAGTGGAGACC 1680  
1621 AGACGAGCAGCCTACGCGCACCCCTGCACTGGGAGAGAGAACATCACAGAGTGGAGACC 1680  
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1741 ATTGCTACGCGCTCAGAGATCACTCTTGCACACCGGAGCGGCTCAAGGGGAGAGTCTTTCGAAC 1800  
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1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTGCGAGGTCCTCAACCATCTGCTGCAT 1860  
1801 GGATCTTGTGAGATATTAATAAAGTTGAGGCTGCGAGGTCCTCAACCATCTGCTGCAT 1860  
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920  
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920  
1921 GGGAACTACACCATTAACAACCTGAGCTCTCCGAGAGGATGAATCGGTGTTGTTCCAT 1980  
1921 GGGAACTACACCATTAACAACCTGAGCTCTCCGAGAGGATGAATCGGTGTTGTTCCAT 1980  
1981 GAGGTGGGCAACTACACGCTTACCTAAGCCAGTGAACCGACTCAACATCAACGAAAG 2040  
1981 GAGGTGGGCAACTACACGCTTACCTAAGCCAGTGAACCGACTCAACATCAACGAAAG 2040  
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2101 GTGCGGGCACCAGGAAGGGATCATCGAGGGGAGCGCCACCTGCTGCTTTGAATGCATG 2160  
2101 GTGCGGGCACCAGGAAGGGATCATCGAGGGGAGCGCCACCTGCTGCTTTGAATGCATG 2160  
2161 GCATCTGACAGGAGAGTTCAGTGAATGAACGATGCAAGTGGTGTACAAAGTGGCCG 2220  
2161 GCATCTGACAGGAGAGTTCAGTGAATGAACGATGCAAGTGGTGTACAAAGTGGCCG 2220  
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2281 TCGTGAAGGAGCCCTTCGGGATCGCTGTGACCATCTTCCGCGTACTGGGATCTGTATC 2340  
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2341 ACCTCTTCTGCTGGGGTCTTTCATCAAGTTTCAGAACTCTCCCATCTGTAAGGCCACC 2400  
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2761 GAGGCTCGCTCATGAGGCTGGGCTTCTCATCGGCTACACCTGCTGCTTCTCGCGGCTC 2820  
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3001 GGGCTGTGGGCTGCTATTTACTTCAACAGTGTGTACATCATCTGTTCAAGCGCTGCGCT 3060  
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3121 GCCACCTCGGCGCAGCGCGGCTTCTGCAAGCGCTTCAAGCGCTGCTGCGCTGCGCT 3180  
3121 GCCACCTCGGCGCAGCGCGGCTTCTGCAAGCGCTTCAAGCGCTGCTGCGCTGCGCT 3180  
3181 ATCTCTGCGCCCTGCTGCTCACTGCGGCGGCTTCAAGCGCTGCTGCGCTGCGCTGCGCT 3240  
3181 ATCTCTGCGCCCTGCTGCTCACTGCGGCGGCTTCAAGCGCTGCTGCGCTGCGCTGCGCT 3240  
3241 AGCACGAGAGGTGCTGCTGAGCGCGGCTTCAAGCGCTGCTGCGCTGCTGCGCTGCGCT 3300  
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3301 ACAGGCGGATACGCCACCTTCAAGCGCGGCTTCAAGCGCTGCTGCGCTGCTGCGCTGCGCT 3360  
3301 ACAGGCGGATACGCCACCTTCAAGCGCGGCTTCAAGCGCTGCTGCGCTGCTGCGCTGCGCT 3360  
3361 AGCGGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420  
3361 AGCGGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420  
3421 CAGCCGCCAAGCATGCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3480













2691	Db		GGGCTTCCTGATCGGCTACACCTGCTGCTGGTGGCATCTGCTCTCTTTGCCCTCAA	2750
2841	Qy		GTCCCGTAAGCTCGCGAGAACTTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTTGAT	2900
2751	Db		GTCCGGAGCTCGCGAGAACTTCATGAAGCCAAGTTTCATCACCTTCAGCATGCTCAT	2810
2901	Qy		CTTCTTCATCGTCTGATCTCTTCATCCCGGCTATGTGAGCACTTACGGCAAGTTTGT	2960
2811	Db		CTTCTTCATCGTCTGGATCTCTTCATTCAGGCTATGCCAGCACCTATGGCAAGTTTGT	2870
2961	Qy		GTCCGCGGTGGAGTGATTCGCATCTTGGCTCCAGCTTCGGGCTGCTGGGCTGCATTTA	3020
2871	Db		CTTGCGGTAGAGTGATTCGCATCTTGGCAGCAGCTTTGGCTTGTGGCTGTCATCTT	2930
3021	Qy		CTTCAACAAGTGTATACATCATCTGTTTCAAGCGTGCGTAAACCATTCAGGAGGTGCG	3080
2931	Db		CTTCAACAAGATCTACATCATTTCTTCAAGCCATCCGCAACACCATTCAGGAGGTGCG	2990
3081	Qy		CTGCAGCAGCGCGGCCACGCTTCAAGTGTGGGCGCGGCGCACCTCGGCGCAGCGC	3140
2991	Db		TTGCAGCAGCGCAGCTCAAGCTTTCAAGTGTGGTGGCGGCGCACGTCGCGCGCAGCAA	3050
3141	Qy		CGGCTCTCGCAAGCGTTCAGCAGCCTGTGCGGCTTCACCATCTCTGCGCCGCTCGTC	3200
3051	Db		CGTCTCCGCAAGGGTTCAGCAGCCTTGAGAGCTCCACGGGATCCACCCCTCTCTCTC	3110
3201	Qy		CACCTGGGCGCGGCTCATCCATGGAGATGCAAGCGTGCAGCAGCAGAGTCAAGTCACTT	3260
3111	Db		CATCAGCAGCAAGAGCAACA-----GCGAAGACCCATTCCACAGCCGAGAGGCAGAAG	3165
3261	Qy		CGGCGGGCACCGTCAACCTGTGCTTCAGCTTCGAGGAGACAGGGCGGATACGCCACCTT	3320
3166	Db		CAGCAGACGGCTGGCCCTTAACCCAGCAAGACGACGACGAGCGCCCTTGAACCTTCCCA	3225
3321	Qy		CAGCCGACAGGCCCGCAGCAGGAACCTGGCGGATGGCCGCAG	3362
3226	Db		CAGCAGCAAGATCTCAGCAGCAGCCAGATGCAAGCAGAAAG	3267

Best Local Similarity	Matches	Conservative	76.4%	0;	Mismatches	658;	Indels	17;	Gaps	3;
501	QY	CTCAGGGTATGGTCCAAACCAAGAGGGCCCGAGAGAGAGACATCATCTACTGGAGGTCT	560							
423	Db	CTCTGCCTACGGGCCAGACCCAGCGAGGCCAAAGAGGGGACATTTATCTTGGGGGCT	482							
561	QY	CTTCCCAATACACTTTGGAGTAGCGGCCAGGATCAGACTTTAAATTCGAGACGGAGGC	620							
483	Db	CTTTCTCTATTCTTTGGAGTAGCAGCTTAAGATCTCAATCAAGGCGCGAGTC	542							
621	QY	GACAAATGTATTCCGTACAATTTTCGAGGCTCCGATGGCTCCAGCGCATGATATTCGC	680							
543	Db	TGTGGAATGTATCAGGTATATTTCCGTGGTTTCGCTGGTTACAGGCTATGATATTTGC	602							
681	QY	AATTGAAGAGATTAAACACATGACTTTCTCCGCCAATATACCTCTGGATATCCCAT	740							
603	Db	CATAGAGGAGATAAACAGCAGCCCGCTTTCTTCCCACTTGACGCTGGGATACAGGAT	662							
741	QY	ATTTCACACAGTGTAAACACCGTGTCCAAAGGCGCTAGAGGCAACACTCAGCTTTGTGGCCCA	800							
663	Db	ATTTCACACTTGCACACCGTTTCTAAGGCGCTTGAAGCCACCTTGATTTTGTGTCTCA	722							
801	QY	GAACAAATTCGACTCGCTGAACTTAGATAGTTCGTAACTGCTCTGACCATATCCCATC	860							
723	Db	AAACAAATTCGACTCGCTGAACTTAGATAGTTCGTAACTGCTCTGACCATATCCCATC	782							
861	QY	CACATATCAGTGGTTCGGGGCAACCGGTCAGGAATCTCCACGCGCTGTGCCAATCTATT	920							
783	Db	TACGATTCTGTGGTGGAGCAATGGCTCAGGGCTTCTCACGGCAGTGGCAATCTGCT	842							
921	QY	GGGATTTATTTACATTCACAGGTCAGCTATGCTCTCTCGAGCAGGCTGTCTCAGCAACA	980							
843	Db	GGGGCTCTTCTACATTTCCAGGTCAGTTAGCTCTCTCAGCAGACTCTCTCAGCAACA	902							

QY 981 GAATGAGTACAGGCTTCTCTGAGGACCATCCCAATGATGAGCAACAGGCCACCGGCCAT 1040  
DB 903 GAATCAATCAAGTCTTTCTCCGAAACCATCCCAATGATGAGCAACAGGCCACCGGCCAT 962  
QY 1041 GCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGAAACCCCTGGCAGCGGACGATGA 1100  
DB 963 GCGAGACATCATCGAGTATTTCCGCTGGAACTGGGTGGGCAAAATGCGAGCTGATGACGA 1022  
QY 1101 CTATGGCCGCCAGGCAATGACAAAGTTCGGGAGGAGGCCGCTTAAGAGGGACATCTGTAT 1160  
DB 1023 CTATGGCGCGCGGGGATTTGAATAATCCGAGAGGAAGCTGAGGAAAGGGATATCTGCAT 1082  
QY 1161 TGACATTCACTGAGATGATCTCTCACTCACTACTACACCCAGAGCAAGTGTGGAGTTTCATCGCCGA 1220  
DB 1083 CGACTTCAGTGAACTCACTCTCCAGTACTCTGATGAGGAAAGATCCAGCATGTGTAGA 1142  
QY 1221 COTCATCCAGAACTCTCTGGCCAAAGGTGATCTGTGTCTTTCTCAANTGCGCCGACCTGGA 1280  
DB 1143 GGTGATTAATAATCCACCGCCAAAGTCACTGTGTGTTTTCTCCAGTGGCCAGATCTTGA 1202  
QY 1281 GCCGCTCATCCAGGAGATGATTCGAGAGAAACATACCGATCGATCTGCTGGCCAGCGA 1340  
DB 1203 GCCCTCATCAAGAGATTTGCCGGGCAATATACGGGCAAGATCTGGCTGGCCAGCGA 1262  
QY 1341 GGCCTGGGCCAGCTCTCTGCTCATTTGCCAAGCCAGAGTACTTCCACGTGGTGGCGGAC 1400  
DB 1263 GGCCTGGGCCAGCTCTCTGCTCATTTGCCAAGCCAGTACTTCCACGTGGTGGCGGAC 1322  
QY 1401 CATCGCTTCGCTCTCAGGGCGGGGGTATCCAGGGTTCACAGGTTTCCATGAGGAGGT 1460  
DB 1323 CATGGATTCTGCTGAAGGCTGGGGCAGATCCAGGGCTTCGGGAAATTCCTGAAGAAGGT 1382  
QY 1461 ACCGCCGCTCAAGGGAGCGCTCAAGCGGGGAACTCCAGCGGACAGCCCTACGCGA 1640  
DB 1383 CCATCCAGGAAGTCTGTCCCAATGGTTTTCGCAAGGAGTTTGGGAAGAAACATTTAA 1442  
QY 1521 CTGCTACTTACCGAGAGACCCCTGACGAGCTGGAAGATTTCCAAAGGTGCCCTCCGACG 1580  
DB 1443 CTGCCACCTTCCAAGA-----AGGTGCAAAAGGACCTTTACCTGTGGACACCTTTCTG 1494  
QY 1581 ACCGGCGCTCAAGGGAGCGCTCAAGCGGGGAACTCCAGCGGACAGCCCTACGCGA 1640  
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QY 1641 CCCCTGCACTGGGAGGAGAAACATCACAGCGTGGAGACCCCTACCTGGATTAACACA 1700  
DB 1551 CCTCTGTACAGGGGATGAACATCAGCAGTGTGAGACCCCTTACATAGATTACACGCA 1610  
QY 1701 CCTGAGGATCTCTACATGATATAGTGGCCGCTTACTCCATTTGCTCAGCCCTGCAAGA 1760  
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QY 1761 CATCCACTCTTGCAAAACCCGGCACCGGCATCTTTGCAACGGATCTTTGTGAGATATTAA 1820  
DB 1671 TATATATACCTGTTACCTGGGAGAGGGCTCTTACCAGTGGCTCTCTGTGAGACATCAA 1730  
QY 1821 AAAAGTTGAGGCTGGCAGGCTCTCAACCATCTGTGATCTGAAGTTTACCAAGCAT 1880  
DB 1731 GAAAGTTGAGGGGTGGCAGGCTCTGAAGCAGCTACGGCATCTTAAACTTTTACAAACAATAT 1790  
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DB 1791 GGGGAGCAGGTTGACCTTTGATGAGTGTGGTGAACCTGTGGGGAACTATTCCATCATCAA 1850  
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DB 1851 CTGGCACCTCTCCGACAGGATGGGTCCATCGTGTTTAAGGAAGTCGGGTATTACAAAGT 1910  
QY 2001 CTACGCTAGCCGAGTGGCCGACTCAACATCAAGGAAGAAATTCCTGGAGTGGCTT 2060  
DB 1911 CTATGCCAAGAGGGGAGAAAGACTCTTTCATCAACGAGGAGAAATTCCTGTGGAGTGGGT 1970

QY 2061 CTCAAAAGTGGTTCTTTCTCCAACTGCGAGTGTGTGCGCGCACACGAGGAGG 2120  
DB 1971 CTCAGGGAGTGGCTTTCTCCAACTGCGAGCCGAGACTGCTGCGAGGACCGAGAAAG 2030  
QY 2121 GATCATCGAGGGGAGGCCACCTGCTGCTTTGTAATGATGCGATGTCGAGAGGAGATT 2180  
DB 2031 GATCATTTAGGGGAGGCCACCTGCTGCTTTGATGTGTGGAGTGTCTGATGGGAGTA 2090  
QY 2181 CAGTGATGAAACGATGCAAGTGTGTACAAAGTGTCCGAAATGATTTCTGTGCGAATGA 2240  
DB 2091 TAGTATGAGACAGATGCCAGTGCCTGTAAACAAGTGTCCAGATGACTTCTGGTCCAAATGA 2150  
QY 2241 GAACCAACACCTGCTGATCGCCAAAGAGATPCGAGTACCTGTCTGTGAOCGAGGCCCTTCGG 2300  
DB 2151 GAACCAACACCTGCTGATTCGCAAGGAGATCGAGTTTCTGTGCGACGAGGCCCTTTGG 2210  
QY 2301 GATCGCTCTGACCATCTTTCGCGCTACTGGGCATCTGTATCACCTCTTCTGTCGTGGGT 2360  
DB 2211 GATCGCACTCACCTCTTTCGCGCTGTGGGCAATTTCTGTACAGCCCTTGTGTGCGGTGT 2270  
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QY 2421 GCTGCTCTTCTCCCTCATCTGCTGCTTCTCCAGCTGCTCATCTTTCATCGGCGAGCCAG 2480  
DB 2331 CTTCTCTTCTCCCTGCTGCTGCTTCTCCAGCTCCCTGCTTCTTTCATCGGGAGCCCA 2390  
QY 2481 GGACTGACCTGTGCGCTCGCCAAACCGGCTTTTGGCATCAGTGTGCTCTGTGCACTCTC 2540  
DB 2391 GGACTGACCTGTGCGCTCGCCAGCGGCTTTTGGCATCAGTGTGCTGCTGCACTCTC 2450  
QY 2541 CTGCATCTCTGTAAGAACCAACCGGGTGTGCTGCTTTCGAGGCGCAAGATTCGCCACAG 2600  
DB 2451 ATGCATCTCTGTAAGAACCAACCGGTGTCTCTCTGCTTGTGAGGCCAAGATTCGCCACAG 2510  
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QY 2661 GGTGCAATCTGTCACCTGCACTCATCTGCTCTACACCGGCTTCTCTCTGCTTCTCTCTGCACTCTC 2720  
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QY 2721 CCATGAGCTGGAGGACAGGTCATCTTTCATCACCTGCGGCGCATCTGCTTCTTCTCTGCTTCTC 2780  
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QY 3081 CTGAGCAGCGGCGGCCACCGCTTCAAGGTGGGGCGCGGCCGCCACCTCTCGCGGCGAGCGC 3140  
DB 2991 TTGAGCAGCGCGAGCTCACTCTTCAAGTGTGCTGCGCGGCCCGCCACCGCTGCGCGCGAGCA 3050  
QY 3141 GCGCTCTCGCAAGCGCTTCCAGAGCGCTGTGGGCTCCACCATCTCTCTGCGCGCGCTCGTC 3200





Db 1203 G C C C T C A T C A G A G A G T T C C G G C C A A T A T C A G G C C A A G A T C T G C T G C C A G C G A 1262  
Qy 1341 G C T T G G G C A G C T C T C C T C A T T G C C A A G C C A G A G T A C T C C A C G T G T G C G G C A C 1400  
Db 1263 G C C T G G G C A G C T C C T C C T G A T G C C A T G C C T C A G T A C T T C C A C G T G T G G G C A C 1322  
Qy 1401 C A T C G G C T T C G C T C A G C G G C G G C G T A T C C A G G T T C A C A A G T T C C T G A A G A G T 1460  
Db 1323 C A T T G A T T C G C T C T G A A G C C T G G G C A G A T C C C A G C T T C C G G A A T T C C T G A A A G A G T 1382  
Qy 1461 C C A C C C C A G A G T C C T C G G A C A A T G G T T T C A A G A G T T C T G G G A G G A C C T T C A A 1520  
Db 1383 C C A T C C C A G A A G T C T G T C C A C A A T G T T T C C A A G A G T T T G G A A A C A C A T T T A A 1442  
Qy 1521 C T G C T A C T T C A C C G A G A A C C C T G A C G A G T G A A G A A T T C C A A G T G C C C T C C A C G G 1580  
Db 1443 C T G C C A C C T C C A A G A - - - - - A G T G C A A A G A G A C C T T T A C C T G T G G A C A C C T T T C T G 1494  
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Db 1495 A G A G G - - - - - T C A G A A A A G T G G G C A C A G T T T A G C A C A G C T C G A C A G C C T T C C G A C C 1550  
Qy 1641 C C C C T G C A C T G G G A G G A A A C A T C A C C A C G T G A G A C C C C C T A C C T G G A T T A T A C A C A 1700  
Db 1551 C C T C T G T A C A G G G A T G A A A C A T C A G C A G T G T C A G A C C C C T T A C A T A G A T T A C A C G C A 1610  
Qy 1701 C T G A G A T C C T C A A T A T A G T A C T G G C C C T A C C A T T G C T C A G C C C T C A G A 1760  
Db 1611 T T T A C G G A T A C C T A C A T G T A C T T A G C A G T C T A C T C C A T T G C C C A G C C C T T C A G A 1670  
Qy 1761 C A T C C A C T T T C A A A C C C G G C A C G G C A T C T T T G C A A C G G A C T T T G T G C A G A T A T T A A 1820  
Db 1671 T A T A T A T A C C T G T T A C C T G G A G A G G C T C T T C A C C A A T G C T C C T G T G C A G A C A T C A A 1730  
Qy 1821 A A A A G T T A G G C C T G C A G G T C C T C A A C C A T C T G T G C A T C T G A A G T T A C C A C A G C A T 1880  
Db 1731 G A A A G T T A G G C C T G C A G G T C C T G A A C C A C C T A C G C A T C T A A A C T T T A C A A A C A A T A T 1790  
Qy 1881 G G T G A C A G G T T G A C T T T G A C A T C A A G T C A C C T C A A G G G A A C T C A C C A T T A T C A A 1940  
Db 1791 G G G G A G C A G G T G A C T T T G A T G A G T G G T G A C T G T G G G A A C T A T T C C A T C A T C A A 1850  
Qy 1941 C T G C A G C T C T C C G A G A G A T G A A T C G G T G T T T C C A T A G G T G G G C A C T A C A A C G C 2000  
Db 1851 C T G G C A C C T C T C C C A G A G A T G G T C C A T C G T G T T T A A G G A A G T C G G G T A T T A C A A G T 1910  
Qy 2001 C T A C C T A A G C C A G T G A C C G A C T C A A C A T C A A C G A A A G A A A T C C T C G A G T G G C T T 2060  
Db 1911 C T A T G C C A A A G G G A A A G A A C T C T T C A T C A A C G A G A G A A A T C C T G T G A G T G G G T T 1970  
Qy 2061 C T C C A A A G T G T T C C T T T C T C C A A C T G C A G T C G A C T G T G C C G G G C A C C A G A A G G 2120  
Db 1971 C T C C A G G A G T G C C C T T C T C C A A C T G C A G C C G A C T G C C T G G C A G G A C C A G A A A G 2030  
Qy 2121 G A T C A T C A G G G G A G C C C A C C T G C T G T T G A A T G C A T G G C A T G T G A G A G G A G A G T T 2180  
Db 2031 G A T C A T T A G G G G A G C C C A C C T G C T G C T T T G A G T G T G G A G T C C T G A T G G G G A G T A 2090  
Qy 2181 C A G T A T A A A C G A T G C A A G T G C G T A C A A A G T G C C C G A A T G A T T C T G T G C A A T G A 2240  
Db 2091 T A G T A T A G A C A G A T G C A G T G C C T G T A A C A A G T G C C C A G A T A C T T C T G T C C A A T G A 2150  
Qy 2241 G A A C C A C A G T C G T G A T C C C A A G A G A T C A G A T C C T G T G T G G A C G A G C C C T T C G G 2300  
Db 2151 G A A C C A C A C C T C T G A T T G C C A A G A G A T C G A G T T C T G T G T G G A C G G A C C C T T T G G 2210  
Qy 2301 G A T C C T C T G A C A C T T C C G C G T A C T G G C A T C C T G A T C A C C T C C T G C T G C G G G T 2360  
Db 2211 G A T G C A C T C A C C C T T T T G C G T G C T G G G A T T T C T G A C A G C C T T T G C T G C G G T 2270  
Qy 2361 C T T C A T C A A G T T C A G A A C A C T C C C A T C G T A A G C C C A C C A C C G G A G T T G T C C A C C T 2420

Db 2271 G T T T A T C A G T T C G C A A C A C A C C C A T T G T C A A G G C C A C C A A C G A G A G C T C T C C T A C C T 2330  
Qy 2421 G C T G C T C T T C C C T C A T C T G C T T C T C A G C T G C T C A T C T T C A T C G C G A G C C C A G 2480  
Db 2331 C C T C C T C T T C C C T G C T G C T T C C A G C T C C T G T T C T T C A T C G G G A G C C C C A 2390  
Qy 2481 G G A C T G A C C T G T C G G C T C G C C A A C G G C T T T G G C A T C A G C T T C G T C C T G T G C A T C T C 2340  
Db 2391 G G A C T G A C G T G C G C C T G C C C A G C C G C C T T T G G A C A G T T C G T G C T G C A T C T C 2450  
Qy 2541 C T G C A T C C T G T G A A G A C C A A C C G G G T G C T G C T T C G A G C C A A A G A T C C C C A C C A G 2600  
Db 2451 A T G C A T C C T G T G A A A C C A A C C G T G C C T C C T G G T T T T G A G C C A A G A T C C C C A C C A G 2510  
Qy 2601 C C T C A C C G A A G T G G G C C T C A C C T G C A G T T C C T C C T G C T T C C T G C A T C C T 2660  
Db 2511 C T T C C A C C G A A G T G G G G G C T C A A C C T G C A G T T C C T G C T G T T T C C T C T G C A C C T T 2570  
Qy 2661 G G T C C A A A T C G T C A C C T G C A T C A T C T G C T A C A C C G C C C T C C C T C C A G C T A C A G A A 2720  
Db 2571 C A T G C A G A T T G T C A T C T G T G A T C T G C C T C A C C G C C C C C C C T C A A G C T A C C G A A 2630  
Qy 2721 C C A T A G C T G A G A C A G A G T C A T C T T C A T C A C C T G G A C A G A G G C T G C T C A T G G G C T 2780  
Db 2631 C C A G A G C T G A G A T A G A T C A T C T T C A T C A G T G C C A C G A G G G C T C C C T C A T G G C C T 2690  
Qy 2781 G G G C T T C C T C A T C G G T A C A C C T G C C C C C C A T C T G T T C T T C T T C G C C T T C A A 2840  
Db 2691 G G G C T T C C T G A T C G G C T A C C C T G C C T G C C C A T C T G C C C A T C T G T T C T T C T T G C C T T C A A 2750  
Qy 2841 G T C C G T A A G C T C C G G A A C T T C A A C A G A G T T A A G T T C A T C A C C T T C A G C A T G T T G A T 2900  
Db 2751 G T C C G G A A G C T G C C G G A A C T T C A A T A A G C C A A G T T C A T C A C C T T C A G C A T G C T C A T 2810  
Qy 2901 C T T C T C A T C T G T G A T C C C T C A T C C C G C C T A T G T C A G C A C C T T A C C G A A G T T G T 2960  
Db 2811 C T T C T C A T C T G T G A T C C C T C A T C C A G C C A T T T G C C T T G C T T G C G T G C A T C T T 2870  
Qy 2961 G T C G C C G T G A G A T G A T T G C C A T C C T G C C T C A G C T T C G G G T G T G C G C T G C A T T T A 3020  
Db 2871 C T C T G C C T A G A G T G A T T G C C A T C C T G C A G C C A G C T T T G C T T G C G T G C A T C T T 2930  
Qy 3021 C T T C A A A G T T A C A T C A T C C T T T C A A G C C G T C C G T A A C A C C A T C A G A G A G T G C G 3080  
Db 2931 C T T C A A A A G A T C A C A T C A T T C T T T C A A G C C A T C C G C A A C C A C C A T C A G A G A G T G C G 2990  
Qy 3081 C T G C A G C A C C G C C C A C C C T T C A A G T G G G C C C G C C C A C C C T C C G G C A G C G C 3140  
Db 2991 T T G C A G C A C C G A G C T C A C C C T T T C A A G T G G T G C C C G G C C A C C G T G C G C G C A A 3050  
Qy 3141 C G C G T C T C G A A G C G T C C A G A C C T G T C G G C T C C A C A T C T C T G C C C C C T G C T 3200  
Db 3051 C G T C C C G C A A G C G G T C C A G A C C T T G A G G C T C C A C G G A T C C A C C C C T C C T C C T C 3110  
Qy 3201 C A C T G C G G C C G G C C T C A C C A T G A G A T G C A G C G T G C A G C A C C A G A G T C A G C T T 3260  
Db 3111 C A T C A G C A G A A G A C A A C A - - - - - G C G A A G A C C A T T C C A C A G C C C A G A G C A A G 3165  
Qy 3261 C G G C A G C C A C C G T C A C C C C T T G C G T C A G C T T C A G A G A C A G G C C G A T A C C C A C C C T 3320  
Db 3166 C A G C A G C A G C C G T G G C C C T A A C C C A G A A G A C A G C A G C A G C A G C C C T G A C C C C C A 3225  
Qy 3321 C A G C C G A C C G C C G A G A G A C T C G G C G A T G C C G C A G 3362  
Db 3226 C A G C A G A A C G A T C T C A G C A G C C C A G A T G A A G A A G 3267

RESULT 12  
US-08-943-986-3  
; Sequence 3, Application US/08943986  
; Patent No. 5962314  
; GENERAL INFORMATION:  
APPLICANT: Edward M. Brown

APPLICANT: Steven C. Hebert  
 APPLICANT: James E. Garrett, Jr.  
 TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
 TITLE OF INVENTION: MOLECULES  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
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 STREET: Suite 4700  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: FASTSEQ  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/943,986  
 FILING DATE: 03-OCT-1997  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/484,565  
 FILING DATE: 7-June-1995  
 APPLICATION NUMBER: 08/353,784  
 FILING DATE: 9 December, 1994  
 APPLICATION NUMBER: PCT/US/94/12117  
 FILING DATE: 21 October, 1994  
 APPLICATION NUMBER: U.S. 08/292,827  
 FILING DATE: 23 August, 1994  
 APPLICATION NUMBER: U.S. 08/141,248  
 FILING DATE: 22 October, 1993  
 APPLICATION NUMBER: U.S. 08/009,389  
 FILING DATE: 23 February, 1993  
 APPLICATION NUMBER: U.S. 08/017,127  
 FILING DATE: 12 February, 1993  
 APPLICATION NUMBER: U.S. 07/934,161  
 FILING DATE: 21 August, 1992  
 APPLICATION NUMBER: U.S. 07/834,044  
 FILING DATE: 11 February, 1992  
 APPLICATION NUMBER: U.S. 07/749,451  
 FILING DATE: 23 August, 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heber, Sheldon O.  
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 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3809 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 373..3606  
 OTHER INFORMATION:  
 US-08-943-986-3

Query Match 42.2%; Score 1745.2; DB 2; Length 3809;  
 Best Local Similarity 76.4%; Pred. No. 0;  
 Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;  
 501 CTCAGGGTATGGTCCAAACCAAGGCGCCAGAGAAAGGAGACATCATACTCGGAGGTCT 560  
 423 CTCTGCTACGGCCAGACCCAGCGAGCCCAAGAGAGGGGGACATTATCTTTGGGGGGCT 482

Qy	561	CTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGACTTTAAATTCAGACCGGAGGC	620
Db	483	CTTTCCTATTCAATTTGGAGTAGCAGCTAAAGATCAAGATCTCAAATCAAGCGCGAGTC	542
Qy	621	GACAAATGATTCGGGTACAAATTTTCGAGGCTTCGATGGCTCCAGGCGGATATATCCG	680
Db	543	TGTGGAATGATCAGGTATAATTTTCGTTGGGTTTCGCTGGTTACAGGCTATGATATTCG	602
Qy	681	AATTTGAAGAGATTAAACAACAGATATGACTTTTCCTGCCCAATATCACCTGGGATATCCGAT	740
Db	503	CATAGAGGAGATAAACAGAGACCCAGCCCTTCTTCCCACTTGACGCTGGGATACAGGAT	662
Qy	741	ATTTGACACGTGTAAACACCGTGTCCAGGGCGGTAGAGGCAACACTCAGCTTTGTGGCCCA	800
Db	663	ATTTGACACTTGCAACACCCGTTTCTAAGGCTTTGGAAGCCACCCCTGAGTTTGTGCTCA	722
Qy	801	GACAAATCGACTCGCTGAACCTTAGATGATGTTCTGTAACTGCTCTGACCATATCCCATC	860
Db	723	AAACAAATTTGATTTCTTGAACTTGTGATGATGTTCTGCACTGCTCAGAGCACATTCCTC	782
Qy	861	CACAATAGCAGTGTGGGGCAACCGGGTCAGGAATCTTCCACGGCTGTGGCCCAATCTATT	920
Db	783	TAGGATTCGCTGTGGTGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAAACTGTCT	842
Qy	921	GGGATTTATTTTACATTCACAGCTCAGCTATGCTCTCTGAGCAGGCTGCTCAGCAACAA	980
Db	843	GGGGCTCTTCTCATTTCCCGAGGTGAGTTAAGCTCTCTCAGCAGACTCTCTCAGCAACAA	902
Qy	981	GATAGGTACAAGGCTTCTCTGAGGACCATCCCAATGATGAGCAACAGGCCACGCCCAT	1040
Db	903	GATCAATTCAGTCTTCTCTCGAACCATTCCCAATGATGAGCAACAGGCCACTGCCAT	962
Qy	1041	GGCGAGATCATGAGCACTTCCAGTGGAACTGGGTGGGAACCTGGCGCCGACCATGA	1100
Db	963	GGCAGACATCATCGAGTATTTCCGCTGGAACTGGGTGGGCAAAATTCGAGCTGATGACGA	1022
Qy	1101	CTATGGCGCCCGAGGCAATTCACAAGTTCCGGGAGGAGGCGCTTAAAGAGGACATCTGTAT	1160
Db	1023	CTATGGCGCGCGGGGATTTGAGAAATTCGAGAGGAGAGCTGAGGAAAGGATATCTGCAT	1082
Qy	1161	TGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAGAGCAGTTGGAGTTATCCGCCGA	1220
Db	1083	CGACTTCAGTGAATCATCTCTCCAGTACTCTGATGAGGAGAGATCCAGCATGTGTAGA	1142
Qy	1221	CGTCATCCAGAACTCTCTGGSCCAAGGTTCATCGTGGTCTTCTCCAAATGGCCCCGACCTGA	1280
Db	1143	GGTGATTCAAAATTCACGGCCAAAGTATCTGTTGTTTCTCCAGTGGGCCAGATCTTGA	1202
Qy	1281	GGCGCTCATCCAGGAGATAGTTTCGGAGAAACATCACCGATCGGATCTGGTGGCCAGCGGA	1340
Db	1203	GGCCCTCATCAAGGAGATTTCCGGGCGCAATATCACGGGCAAGATTCGGTGGCCAGCGGA	1262
Qy	1341	GGCTTGGCCAGCTCTTCGCTCATTCGCAAGCAGAGTACTTCCAGTGGTGGCGCGCAC	1400
Db	1263	GGCTTGGCCAGCTCTTCGCTCATTCGCAAGCAGAGTACTTCCAGTGGTGGCGCGCAC	1322
Qy	1401	CATCGGCTTCGCTCTCAGGGCGGGCGGTATCCAGGGGTTCAACAAGTTCTCTGAAGAGGT	1460
Db	1323	CATTGGATTGCTCTGAGGCTGGGAGATCCAGAGGCTTCGGGGAATTCCTGAAGAAGGT	1382
Qy	1461	CCACCCAGCAGGTCTCCGAGCAATGGGTTGTCAAGGAGTTCTGGAGAGAGACCTTCAA	1520
Db	1383	CCATCCAGGAAAGTCTGTCCACAATGGTTTTCGCAAGGAGTTTGGGAAGAAACATTAA	1442
Qy	1521	CTGCTACTTCCGAGAGAGACCTCTGACGAGCTGAAGAATTCGAAGGTGCGCTCGCACGG	1580
Db	1443	CTGCCACTTCAAGA-----AGTGTCAAAGGACCTTTACTGTGGACACCTTTCTG	1494
Qy	1581	ACCGCGGCTCAAGGGGACCGCTCCAAAGGCGGGGAATCCAGAGGAGACCCCTTAGCCCA	1640
Db	1495	AGAGG----TCAAGAAAGAGTGGCGACAGGTTTAGCAACAGCTCGACAGCCTTCCGACC	1550
Qy	1641	CCCCTGCACTGGGAGGAGAGACATCACCGGTGAGACCCCTTACTCTGGATTATACACA	1700

1551 DB CTTCTGTACAGGGATGAGACATCAGCAGTGTGAGAGCCCTTACATAGATTACAGCA 1610  
 1701 QY CTTGAGGATCTCTCAATATATACGTCGCGCGTCTACTCCATGCTCAGCGCTTCAAGA 1760  
 1611 DB TTACGGATATCTCAATATGTTACTTACAGTCTACTCCATGTCGCGCGCTTCAAGA 1670  
 1761 QY CATCACTCTTCAAAACCGGACCGGATCTTTGCAACAGGATCTTGTGAGATATTAA 1820  
 1671 DB TATATATACCTGTTACTTGGAGAGGGCTCTTACCAATGCTCTGTGAGACATCAA 1730  
 1821 QY AAAAGTGAAGGCTGGAGGCTCTCAACATCTGTGATCTGAAGTTTACACAGCAT 1880  
 1731 DB GAAAGTGAAGGCTGGAGGCTCTCAACAGCATCTGAGGATCTTAAACTTTACAAACAATAT 1790  
 1881 QY GGGTGAAGGCTGGAGGCTCTCAACAGCATCTGAGGATCTTAAACTTTACAAACAATAT 1940  
 1791 DB GGGGAGGAGGCTGGAGGCTCTCAACAGCATCTGAGGATCTTAAACTTTACAAACAATAT 1850  
 1941 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2000  
 1851 DB CTTGACCTCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 1910  
 2001 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2060  
 1911 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 1970  
 2061 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2120  
 1971 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2030  
 2121 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2180  
 2031 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2090  
 2181 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2240  
 2091 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2150  
 2241 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2300  
 2151 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2210  
 2301 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2360  
 2211 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2270  
 2361 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2420  
 2271 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2330  
 2421 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2480  
 2331 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2390  
 2481 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2540  
 2391 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2450  
 2541 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2600  
 2451 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2510  
 2601 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2660  
 2511 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2570  
 2661 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2720  
 2571 DB CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2630  
 2721 QY CTTGAGGCTCTCGGAGGATGAAATCGGTGTTTCCATGAGTGGGCAACTACAACGC 2780

2631 DB CCAGGAGCTGGAGGATGAGATCATCTTATCATCGTCCAGGAGGCTCCCTCATGCGCCT 2690  
 2781 QY GGGCTTCTCATCGGCTACACCTGCTCTCGCGGCTCTCTCTCTCTCTCTCTCTCTCTCA 2840  
 2691 DB GGGCTTCTCATCGGCTACACCTGCTCTCGCGGCTCTCTCTCTCTCTCTCTCTCTCA 2750  
 2841 QY GTCCGTAAGCTCCGAGAACTTCAACGAGGTAAGTTTATCACCTTACAGATGTTGAT 2900  
 2751 DB GTCCGTAAGCTCCGAGAACTTCAACGAGGTAAGTTTATCACCTTACAGATGTTGAT 2810  
 2901 QY GTTCTTATGCTGTGATCT 2960  
 2811 DB GTTCTTATGCTGTGATCT 2870  
 2961 QY GTTCTTATGCTGTGATCT 3020  
 2871 DB GTTCTTATGCTGTGATCT 2930  
 3021 QY GTTCTTATGCTGTGATCT 3080  
 2931 DB GTTCTTATGCTGTGATCT 2990  
 3081 QY GTTCTTATGCTGTGATCT 3140  
 2991 DB GTTCTTATGCTGTGATCT 3050  
 3141 QY GTTCTTATGCTGTGATCT 3200  
 3051 DB GTTCTTATGCTGTGATCT 3110  
 3201 QY GTTCTTATGCTGTGATCT 3260  
 3111 DB GTTCTTATGCTGTGATCT 3165  
 3261 QY GTTCTTATGCTGTGATCT 3320  
 3166 DB GTTCTTATGCTGTGATCT 3325  
 3321 QY GTTCTTATGCTGTGATCT 3362  
 3326 DB GTTCTTATGCTGTGATCT 3267

RESULT 13  
 US-08-353-784-3  
 ; Sequence 3, Application US/08353784  
 ; Patent No. 6011068  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edward F. Nemeth, Edward M.  
 ; APPLICANT: Brown, Steven C. Hebert,  
 ; APPLICANT: Bradford C. Van Wagenen, Manuel  
 ; APPLICANT: F. Balandrin, Forrest H. Fuller,  
 ; APPLICANT: Eric G. DelMar, and Scott T. Moe  
 ; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
 ; TITLE OF INVENTION: MOLECULES  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: First Interstate World Center  
 ; STREET: Suite 4700  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: FASTSEQ  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/353,784  
 ; FILING DATE: 9 December, 1994

CLASSIFICATION: 514  
 PRIOR APPLICATION DATA: including application  
 PRIOR APPLICATION DATA: described below: 8  
 PRIOR APPLICATION DATA: described below: 8  
 FILING DATE: 21 October, 1994  
 APPLICATION NUMBER: PCT/US/94/12117  
 FILING DATE: 21 October, 1994  
 APPLICATION NUMBER: U.S. 08/292,827  
 FILING DATE: 23 August, 1994  
 APPLICATION NUMBER: U.S. 08/141,248  
 FILING DATE: 22 October, 1993  
 APPLICATION NUMBER: U.S. 08/009,389  
 FILING DATE: 23 February, 1993  
 APPLICATION NUMBER: U.S. 08/017,127  
 FILING DATE: 12 February, 1993  
 APPLICATION NUMBER: U.S. 07/934,161  
 FILING DATE: 21 August, 1992  
 APPLICATION NUMBER: U.S. 07/834,044  
 FILING DATE: 11 February, 1992  
 APPLICATION NUMBER: U.S. 07/749,451  
 FILING DATE: 23 August, 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heber, Sheldon O.  
 REGISTRATION NUMBER: 38,179  
 REFERENCE/DOCKET NUMBER: 209/069  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510

## INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 3809 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 373..3606  
 OTHER INFORMATION:  
 US-08-353-784-3

Query Match 42.2%; Score 1745.2; DB 3; Length 3809;  
 Best Local Similarity 76.4%; P: Mismatches 658; Indels 17; Gaps 3;  
 Matches 2187; Conservative 0

QY	501	CTCAGGCTATGGTCCAAACCAAGGCCCCAGAGAAAGGAGACATCATCTGGAGGTCT	560
DB	423	CTCTGCTACGGCCAGACCCAGGAGCCCAAGAGGGGACATTTCTTTGGGGGCT	482
QY	561	CTTCCCAATACATTTGGAGTAGCCGCCAAGGATCAGGACTTAAATCGAGACCGGAGGC	620
DB	483	CTTTCTTATTCATTTGGAGTAGCAGCTAAAGATCTCAAATCAAGGCCCGGAGTC	542
QY	621	GACAAATGATTCGGTACAAATTTCCAGGCTTCGATGGCTCCAGGGGATGATATTCGC	680
DB	543	TGTGGAATGTATCAGGTATTAATTTCCGTTGGGTTTCTGTTTACAGGCTATGATATTCG	602
QY	681	AATTTGAAGAGATTAACACAGTATGATCTTCTGCCCCAATATCACCTGGGATATCGCAT	740
DB	603	CATAGAGGAGATAAACAGAGCCAGCCCTCTTCCCACTTGAGCTGGGATACAGAT	662
QY	741	ATTGACAGTGTAAACACCGTGTCCAGGCGGTAGAGCAACACTCAGCTTTGTGGCCCA	800
DB	663	ATTGACACTTGAACACCGCTTTCTAAGGCCCTTGAAGCCACCCCTGAGTTTGTGCTCA	722
QY	801	GAACAAATTCGACTCGCTGAACTTAGATGATTTCTGTAACTGCTCTGACCATATCCCATC	860
DB	723	AAACAAATTTGATCTTTGAACTTGATGATTCGAACTGCTCTGACGACCATTTCCCTC	782
QY	861	CACATAGCAGTGGTGGGGCAACCGGTCAGGAATCTCCAGGCTGTGGCCAAATCTATT	920
DB	783	TACGATTGCTGTGGTGGGAGCAACTGGCTCAGGCGTCTCCACGGCAGTGGCAATCTGCT	842

QY	921	GGGATTTATTTTACATTCACAGGTCCAGCTATGCTCTCGAGCAGGCTCTCAGCAACAA	980
DB	843	GGGGCTCTTCTTACATTCCTCCAGGTCTAGTTAAGCTCTCTCCAGCAGACTCTCAGCAACAA	902
QY	981	GAATGAGTACAAGGCTTCTCTGAGGACCATCCCAATGATGAGCAACAGGCCACGCGCAT	1040
DB	903	GAATCAATTCAGTCTTTCTCCGAAACCATCCCAATGATGAGCAACAGGCCACTGCCAT	962
QY	1041	GGCCGAGATCATCGACACTTCCAGTGGAACTGGGTGGGAACCTGGCAGCCGACCATGA	1100
DB	963	GGCAGACATCATCGAGTATTTCCGCTGGAACTGGGTGGGCACAATTCGAGCTGATGACGA	1022
QY	1101	CTATGGCCGCCAGGCAATTCACAAGTTCCGGGAGGAGCGGTAAAGAGGGACATCTGTAT	1160
DB	1023	CTATGGGGCCGGGATTTGAGAAATTCGAGAGGAGCTGAGGAAAGGATATCTGCAT	1082
QY	1161	TGACTTCAGTGAAGATGATCTCTCAGTACTACACCCAGAGACGTTGGAGTTTCACTGCCGA	1220
DB	1083	CGACTTCAGTGAATCTCTCTCCAGTACTCTGATGAGGAAGATCCAGCATGTGTAGA	1142
QY	1221	CGTCATCCAGAACTCTCTCGGCCAAGGTCTCGTGTCTCTCCAAATGGCCCCGACCTGGA	1280
DB	1143	GGTGATTTCAAAATTCACGGCCAAAGTCTCGTGTCTCTCCAGTGGGCCAGATCTTGA	1202
QY	1281	GGCGCTCATCCAGGAGATAGTTCCGAGAAACATCAACCGATCGGATCTGGCTGGCCAGCA	1340
DB	1203	GGCCCTCATCAAGGAGATTTCCGGGCCAATATCAACGGGCAAGATCTGGCTGGCCAGCA	1262
QY	1341	GGCTTGGCCAGCTCTTCGCTCATTCGCCAGCCAGAGTACTTCCAGTGGTGGCGGCAC	1400
DB	1263	GGCTTGGCCAGCTCTTCGCTCATTCGCCAGCCAGTACTTCCAGTGGTGGCGGCAC	1322
QY	1401	CATCGGCTTCGCTCTCAGGGCGGGGCTATCCAGGGTTCAACAAGTTCTTGAAGAGGT	1460
DB	1323	CATTTGATTCGCTCTGAGGCTGGCCAGATCCAGGCTTCCGGGAATCTCTGAAGAGGT	1382
QY	1461	CCACCCAGCAGGTCTCCGACAAATGGTGTTCAGGAGTCTTCGGAGGAGACCTTCAA	1520
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QY	1641	CCCTCGACTGGGGAGGAGAACATCACCGCTGGAGACCCCTACTCTGATTTATACACA	1700
DB	1551	CCTCTGTACAGGGAGTGAAGAACATCAGAGTGTGAGACCCCTTACATGATTACAGCA	1510
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DB	1671	TATATATACCTGTCTTACCTGGGAGGGCTCTTCAACCAATGGCTCTGTGACACATCAA	1730
QY	1821	AAAAGTTGAGGCTTGGCAGGTCTCTCAACCATCTGTGTCATCTGAAGTTTACCAACAGCAT	1880
DB	1731	GAAAGTTGAGGCTTGGCAGGTCTCTGAAGCACCTTACGGCATCTAACTTTTACAAACATAT	1790
QY	1881	GGGTGACAGGTTGACTTTGACGATCAAGGTGACCTCAGAGGGAACCTACACCATTTTCAA	1940
DB	1791	GGGGGACAGGTGACCTTTGATGAGTGTGTGACCTGGTGGGGAACCTATTTCCATCATCAA	1850
QY	1941	CTGGCAGCTCTCCGACAGGAGTGAATCGGTGTGTGTTCATGAGTGGGGAACCTACCAACGC	2000
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/ REFERENCE/DOCKET NUMBER: 213/007  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (213) 489-1600  
/ TELEFAX: (213) 955-0440  
/ TELEX: 67-3510  
/ INFORMATION FOR SEQ ID NO: 3:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 3809 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: cDNA to mRNA  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: 373..3606  
/ US-08-484-719B-3

Query Match 42.2%; Score 1745.2; DB 3; Length 3809;  
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DB	483	CTTTCCTATTCAATTTGGAGTAGCAGCTAAAGATCAAGATCTCAATCAAGGCCGAGTC	542
QY	621	GACAAATATATTTCGGTACAAATTTTCGAGGCTTCGAGTGGCTCCAGGGGATGATTCGC	680
DB	543	TGTGGATGATACAGGTAAATTTCCGTGGGTTTCGTGGTTTACAGGCTATGATATTGC	602
QY	681	AATTGAGAGATTAACAACAGTATGACTTCTCGGCCAATATACCCCTGGGATATCGCAT	740
DB	603	CATAGAGGAGATAAACAGACGCGCCAGCCCTTCTCCCAATGTACGCTGGGATACAGAT	662
QY	741	ATTTGACAGCTGTAAACACCGCTGTCAAGCGCTAGAGGCAACACTCAGCTTGTGGCCCA	800
DB	663	ATTGACACTTGCACACCGCTTCTAAGGCTTGAAGGCCACCTGAGTTTGTGTCTCA	722
QY	801	GAAACAAATCGACTCGCTGAACTTAGATGAGTTCTGTAACTGCTGTGACCATATCCCATC	860
DB	723	AAACAAATTTGATTTCTTTGAACCTTGTAGTGTCTGCAACTGCTCAGAGCAATTCCTCTC	782
QY	861	CACATAGCAGTGTGGGGCAACCGGTCAGGAATCTCCAGGCTGTGGCCAACTATT	920
DB	783	TACGATTGCTGTGGGAGCAACTGGCTCAGGCGTCTCCAGCGAGTGGCAATCTGCT	842
QY	921	GGGATTTATTTACATTCACAGGTGAGCTATGCCCTCTCGAGCAGGCTGCTCAGCAACA	980
DB	843	GGGGCTCTTCTACATTCCTCCAGGTGAGTTATGCCCTCTCCAGCAGACTCCTCAGCAACA	902
QY	981	GAAATGATACAGGCTTCTCAGAGCAATCCCAATGATGAGCAACAGCCAGCCAGCCAT	1040
DB	903	GAAATCAATTCAGTCTTCTCCGAAACCAATCCCAATGATGAGCAACAGCCAGCCAGCCAT	962
QY	1041	GGCCGAGATCATCGAGCACTTCAGTGGAACTGGGTGGGAAACCTTGGCAGCGCAGCATGA	1100
DB	963	GGCAGACATCATGAGTATTTCCGTGGAACTGGGTGGGCAATTTGACAGCTGATGAGCA	1022
QY	1101	CTATGGCCGCCAGGATTTGACAGTTTCGGGAGAGAGCGGTTAAGAGGCAATCTGTAT	1160
DB	1023	CTATGGGCGCGGGGATTTGAGAAATTCGAGAGGAGCTGAGGAAGGAGATATCTGCAT	1082
QY	1161	TGACTTTCAGTGAGATGATCTCTCAGTACTACACCCAGAGAGAGTTGGAGTTTCATCGCCGA	1220
DB	1083	CGACTTCAGTGAATCATCTCCAGTACTCTGATGAGGAAGAGATCCAGCATGTGGTAGA	1142
QY	1221	CGTATCCAGAACTCTCGGCCAAAGGTATATGTGTCTTCTCAATGGCCCCGAGCTTGA	1280
DB	1143	GGTGATTCAAAATTCACGCGCAAAAGTATCTGTGGTTTCTCCAGTGGGCCAGATCTTGA	1202

QY	1281	GCCCTCATCCAGGAGATAGTTCCGAGAAACATCACCGATCGATCTGCTGGCCAGCA	1340
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QY	1581	ACGGGGCTCAAGGGGACGGCTCCAGGGCGGGAATCCAGACGAGACGCGCTAGCCCA	1640
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DB	1551	CTCTGTACAGGGGATGAGAACATCAGCAGTGTGAGAGCCCTTACATAGATTACAGCA	1610
QY	1701	CTTGAGGATCTCTCAATGTATATCGTGGCGTCTACTCATGCTCAGCGCTTGCACAGA	1760
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DB	1731	GAAAGTTGAGGCTGTCAGTCTCTCAACATCTGTGTCATCTGAAGTTTACCAACATAT	1790
QY	1881	GGGTGAGAGGTTGACTTTGACGATCAAGTGACCTCAGGGGAACTACACCATATCAA	1940
DB	1791	GGGGAGAGAGTGACCTTTGATGAGTGTGACCTGTGGGAACTATTCATCATCAA	1850
QY	1941	CTGGCAGCTCTCCGAGAGAGTGAATCGGTGTTGTTTCCATGAGTGGGCACTACACGC	2000
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QY	2061	CTCAAAAGTGGTCTCTTCTCCAACTGCACTCGAGTGTGCTGCCGGGCAACAGGAGGG	2120
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RESULT 15  
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; Sequence 2, Application US/08546998  
; Patent No. 6211244  
; GENERAL INFORMATION:

APPLICANT: Van Wagenen, Bradford C.  
APPLICANT: Moe, Scott T.  
APPLICANT: Balandrin, Manuel F.  
APPLICANT: DelMar, Eric G.  
APPLICANT: Nemeth, Edward F.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: COMPOUNDS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/546,998  
FILING DATE: October 23, 1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 215/304  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 499-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3809 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 373...3606  
OTHER INFORMATION:  
US-08-546-998-2

Query Match 42.2%; Score 1745.2; DB 3; Length 3809;  
Best Local Similarity 76.4%; Pred. No. 0;  
Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;  
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	4134	100.0	4134	15	US-10-270-876-17
6	4134	100.0	4134	15	US-10-268-051-7
7	4134	100.0	4134	15	US-10-125-772-1
8	4134	100.0	4134	15	US-10-016-496-1
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16	1678.2	40.6	4113	16	US-10-152-319A-1632	Sequence 1632, Ap
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18	1418.6	34.3	3941	14	US-10-125-778-7	Sequence 7, Appli
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ALIGNMENTS

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; Sequence 17, Application US/09975553  
; Patent No. US20020152968A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, H. William, Jr.  
; APPLICANT: Russell, David R.  
; APPLICANT: Nearing, Jacqueline  
; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous  
; TITLE OF INVENTION: Fish  
; FILE REFERENCE: 2213.1004-001  
; CURRENT APPLICATION NUMBER: US/09/975.553  
; CURRENT FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 09/687,477  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 09/687,476  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 09/687,372  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 4134  
; TYPE: DNA  
; ORGANISM: Dogfish Shark  
US-09-975-553-17

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; Sequence 1, Application US/10125792  
; Publication No. US20030051269A1  
; GENERAL INFORMATION:  
; APPLICANT: MariCal  
; APPLICANT: Harris, H. William  
; APPLICANT: Nearing, Jacqueline A.  
; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
; FILE REFERENCE: 2213.1006-007  
; CURRENT APPLICATION NUMBER: US/10/125,792  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 10/121,441  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US01/31704  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 60/240,392

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; PRIOR FILING DATE: 2000-10-12
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; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-792-1

Query Match      100.0%; Score 4134; DB 14; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1501 TTCTGGGAGGAGACCTTCAACTGCTACTTCCAGGAGAGACCTCTGACGAGCTGAAGAAT 1560
1561 TCCAAAGTGGCTCGACGAGACCGGCTCAGGAGACCGCTCCAGGCGGGGAACTCC 1620
1561 TCCAAAGTGGCTCGACGAGACCGGCTCAGGAGACCGCTCCAGGCGGGGAACTCC 1620
1621 AGACGACAGCCCTTACGCCACCCCTGCACTGGGAGAGAGAACATCAACAGCTGGAGACC 1680
1621 AGACGACAGCCCTTACGCCACCCCTGCACTGGGAGAGAGAACATCAACAGCTGGAGACC 1680
1681 CCTTACCTGGATTTATACACACTGAGGATCTCTTACAAATGATATACGTTGGCTCTACTCC 1740
1681 CCTTACCTGGATTTATACACACTGAGGATCTCTTACAAATGATATACGTTGGCTCTACTCC 1740
1741 ATTCTCAGCCCTTGAAGACATCCACTTTTGAACCCCGGACCGGCACTTTTGAACAC 1800
1741 ATTCTCAGCCCTTGAAGACATCCACTTTTGAACCCCGGACCGGCACTTTTGAACAC 1800
1801 GGATCTTGTGAGATATTTAAAAAGTTGAGGCTTGGCAGTCTCTCAACATCTGCTGCAT 1860
1801 GGATCTTGTGAGATATTTAAAAAGTTGAGGCTTGGCAGTCTCTCAACATCTGCTGCAT 1860
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTCAGCATCAAGTCAAGTCAAG 1920
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTCAGCATCAAGTCAAGTCAAG 1920
1921 GGGAACTACACCATTTCAACTGGCAGCTCTCCGACAGGATGAATCGGTGTTGTTCCAT 1980
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## RESULT 3

US-10-125-778-1  
; Sequence 1, Application US/10125778  
; Publication No. US20030082574A1  
; GENERAL INFORMATION:  
; APPLICANT: Marical  
; APPLICANT: Harris, H. William  
; APPLICANT: Nearing, Jacqueline A.  
; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
; FILE REFERENCE: 2213.1006-005  
; CURRENT APPLICATION NUMBER: US/10/125,778  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 10/121,441  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US01/31704  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR APPLICATION NUMBER: 60/240,392  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/240,003  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4134  
; TYPE: DNA  
; ORGANISM: Squalus acanthias  
US-10-125-778-1

Query Match 100.0%; Score 4134; DB 14; Length 4134;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	GCATTACAGGAACATGCACTACATCTGTGTTAATGAATATGTCAGTTATCTGAAGT	120
DB	61	GCATTACAGGAACATGCACTACATCTGTGTTAATGAATATGTCAGTTATCTGAAGT	120
QY	121	TATTAATAATGTTTCTCAAGGATGGCTTCCAGAGAAATCAATCTGCAGCTTTTCCCAT	180
DB	121	TATTAATAATGTTTCTCAAGGATGGCTTCCAGAGAAATCAATCTGCAGCTTTTCCCAT	180
QY	181	GTCAATTGTATGAATACTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGACCA	240
DB	181	GTCAATTGTATGAATACTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGACCA	240
QY	241	GTTCAACCTTCTTGAGGATAGATCAACCTGAGGAGATGGAAGCTTCAGAGGAA	300
DB	241	GTTCAACCTTCTTGAGGATAGATCAACCTGAGGAGATGGAAGCTTCAGAGGAA	300
QY	301	ATGGGATGATCTTCAGGAGTTCGTGTAAAGCGATCCCTCACCATTACAAAGATAA	360
DB	301	ATGGGATGATCTTCAGGAGTTCGTGTAAAGCGATCCCTCACCATTACAAAGATAA	360
QY	361	GCAGAAATCTTCAGGATCTGTAAAGGGCTGGCTAGTGTGGCTTGGTCAAGGAA	420
DB	361	GCAGAAATCTTCAGGATCTGTAAAGGGCTGGCTAGTGTGGCTTGGTCAAGGAA	420
QY	421	CAGAGACAGGGCTGCACATGGCTCAGCTTCACTGCAACTCTTATCTTGGGATTTACA	480
DB	421	CAGAGACAGGGCTGCACATGGCTCAGCTTCACTGCAACTCTTATCTTGGGATTTACA	480
QY	481	CTCCTACAGTCGTAATGTCTCAGGGATGTGTCACAAACCAAGGGCCAGAGAAAGGA	540
DB	481	CTCCTACAGTCGTAATGTCTCAGGGATGTGTCACAAACCAAGGGCCAGAGAAAGGA	540
QY	541	GACATCATCTGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC	600
DB	541	GACATCATCTGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC	600

QY	601	TTAAATCGAGACCGGAGCGCAAAATGTATTCGGTACAAATTTTCAGGCTTCCGATGG	660
DB	601	TTAAATCGAGACCGGAGCGCAAAATGTATTCGGTACAAATTTTCAGGCTTCCGATGG	660
QY	661	CTCCAGGCGATGATATTTCGCAATTGAAGATTAACAAACAGTATGACTTCTCCGCCAAT	720
DB	661	CTCCAGGCGATGATATTTCGCAATTGAAGATTAACAAACAGTATGACTTCTCCGCCAAT	720
QY	721	ATCACCTCGGATATGCAATATTGACACGTGTAAACACCGTGTCCAAAGGCGCTAGAGGCA	780
DB	721	ATCACCTCGGATATGCAATATTGACACGTGTAAACACCGTGTCCAAAGGCGCTAGAGGCA	780
QY	781	ACACTCAGCTTTGTGGCCAGAAACAAATTCGCTCGTGAACCTTAGATGAGTTCTGTAA	840
DB	781	ACACTCAGCTTTGTGGCCAGAAACAAATTCGCTCGTGAACCTTAGATGAGTTCTGTAA	840
QY	841	TGCTCTGACCATATCCCATCCCAATAGCAGTGGTGGGCAACCGGCTCAGGAATCTCC	900
DB	841	TGCTCTGACCATATCCCATCCCAATAGCAGTGGTGGGCAACCGGCTCAGGAATCTCC	900
QY	901	ACGGCTGTGGCCAAATCTATTGGGATTTATTTACATTCACAGCTCAGCTATGCTCTCG	960
DB	901	ACGGCTGTGGCCAAATCTATTGGGATTTATTTACATTCACAGCTCAGCTATGCTCTCG	960
QY	961	AGCAGGCTGCTCAGCAACAGAAATGAGTACAGGCTTCTCGAGGACCATCCCAATGAT	1020
DB	961	AGCAGGCTGCTCAGCAACAGAAATGAGTACAGGCTTCTCGAGGACCATCCCAATGAT	1020
QY	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080
DB	1021	GAGCAACAGGCCACGGCCATGGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080
QY	1081	ACCTGCGACCGCAAGATGACTATGGCCGCCAGGATTTGCAAGTTCCGGGAGGAGGC	1140
DB	1081	ACCTGCGACCGCAAGATGACTATGGCCGCCAGGATTTGCAAGTTCCGGGAGGAGGC	1140
QY	1141	GTTAAGAGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG	1200
DB	1141	GTTAAGAGGACATCTGTATTGACTTCAGTGAGATGATCTCTCAGTACTACACCCAGAAG	1200
QY	1201	CAGTTGAGTTCAATCGCCGACGTCAATCCAGAACTCTCGGCCAAGGTCACTGCTGCTTC	1260
DB	1201	CAGTTGAGTTCAATCGCCGACGTCAATCCAGAACTCTCTCGGCCAAGGTCACTGCTGCTTC	1260
QY	1261	TCCAAATGCGCCGACCTGAGGAGCGCTCATCCAGAGATAGTTCCGAGAAACATCAACGAT	1320
DB	1261	TCCAAATGCGCCGACCTGAGGAGCGCTCATCCAGAGATAGTTCCGAGAAACATCAACGAT	1320
QY	1321	CGGATCTGGTGGCCACGAGGCTTGGGCGAGCTCTTCGCTCAATGCCAAGCCAGAGTAC	1380
DB	1321	CGGATCTGGTGGCCACGAGGCTTGGGCGAGCTCTTCGCTCAATGCCAAGCCAGAGTAC	1380
QY	1381	TTCCAGTGTGGCGGACCATCGGCTTCGCTCTCAGGGCGGGGTATCCCGAGGTTTC	1440
DB	1381	TTCCAGTGTGGCGGACCATCGGCTTCGCTCTCAGGGCGGGGTATCCCGAGGTTTC	1440
QY	1441	AACAAGTTCTGAAGAGAGTCCACCCGAGAGTCTTCGAGCAATGGGTTGTCAAGGAG	1500
DB	1441	AACAAGTTCTGAAGAGAGTCCACCCGAGAGTCTTCGAGCAATGGGTTGTCAAGGAG	1500
QY	1501	TTCTGGAGGAGACCTTCAACTGCTACTTCCGAGAGAACCTTGACGAGCTGAAGAAT	1560
DB	1501	TTCTGGAGGAGACCTTCAACTGCTACTTCCGAGAGAACCTTGACGAGCTGAAGAAT	1560
QY	1561	TCCAGGCTGCTCGACCGACCGGCGCTCAAGGGAGCGGCTCCAGGGCGGGAATCTCC	1620
DB	1561	TCCAGGCTGCTCGACCGACCGGCGCTCAAGGGAGCGGCTCCAGGGCGGGAATCTCC	1620
QY	1621	AGACGGAACAGCCCTTACGCCACCCCTGCACTGGGGAGGAGAAATCAACAGCTGGAGAC	1680
DB	1621	AGACGGAACAGCCCTTACGCCACCCCTGCACTGGGGAGGAGAAATCAACAGCTGGAGAC	1680
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Db 4021 TGTAAATCAGATGTGTAATTTGGTAAATTTCTCTGTACATTAATGCAATTTCTTGATA 4080
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RESULT 4
US-10-270-795-17
; Sequence 17, Application US/10270795
; Publication No. US20030084855A1
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; FILE OF INVENTION: Fish
; FILE REFERENCE: 2213.2002-000
; CURRENT FILING DATE: US/10/270,795
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,372
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-795-17

Query Match 100.0%; Score 4134; DB 14; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTCGGTTGCTGCTCGGTTTCAGTCCAGAGTCTCTCCAGTGCAAAATGGAATGGTGTGC 60
Db 1 AATTCGGTTGCTGCTCGGTTTCAGTCCAGAGTCTCTCCAGTGCAAAATGGAATGGTGTGC 60
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1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920  
1861 CTGAAGTTTACCAACAGCATGGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAG 1920  
1921 GGGAACTACACATTATCAACTGGCAGCTCCGAGAGGATGAATCGGTGTGTTCCAT 1980  
1921 GGGAACTACACATTATCAACTGGCAGCTCCGAGAGGATGAATCGGTGTGTTCCAT 1980  
1981 GAGGTGGGCAACTACAAACCCCTACGCTAAGCCCACTGACCGACTCAACATCAAGAAAG 2040  
1981 GAGGTGGGCAACTACAAACCCCTACGCTAAGCCCACTGACCGACTCAACATCAAGAAAG 2040  
2041 AAAATCCTCTGAGTGGCTTCTCAAAAGTGTTCTTCTCCAACTGAGTGGTGTGTTCCAT 2100  
2041 AAAATCCTCTGAGTGGCTTCTCAAAAGTGTTCTTCTCCAACTGAGTGGTGTGTTCCAT 2100  
2101 GTGCGGGGACCAAGGAGGGATCTCGAGGGGAGCCACCTGCTTGAATGCAATG 2160  
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2161 GCATGTGCAGAGGAGTTCACTGATGATAAAGATGCAAGTGCCTGATCAAAAGTGCCCG 2220  
2161 GCATGTGCAGAGGAGTTCACTGATGATAAAGATGCAAGTGCCTGATCAAAAGTGCCCG 2220  
2221 AATGATTTCTGTCGAATGAGAACCACTGCTGATCGCATCGCAAGGAGATCGAGTACCTG 2280  
2221 AATGATTTCTGTCGAATGAGAACCACTGCTGATCGCATCGCAAGGAGATCGAGTACCTG 2280  
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2341 ACCTCCTTCTGCTGGGCTTCTCAAGTTGAGAAACACTCCCATCGTGAAGGCCACC 2400  
2341 ACCTCCTTCTGCTGGGCTTCTCAAGTTGAGAAACACTCCCATCGTGAAGGCCACC 2400  
2401 AACCGGAGTTGCTTCACTGCTGCTTCTCCCTCATCTGCTTCTCCAGCTCGCTC 2460  
2401 AACCGGAGTTGCTTCACTGCTGCTTCTCCCTCATCTGCTTCTCCAGCTCGCTC 2460  
2461 ATCTTATCGGAGCCAGGACTGGACTGTGCGCTCCGCCAACCGGCTTTGGCATC 2520  
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2521 AGCTTCGTCTGTGATCTCTCTGATCTCTGAGAACCAACCGGCTGTGCTGCTTTC 2580  
2521 AGCTTCGTCTGTGATCTCTCTGATCTCTGAGAACCAACCGGCTGTGCTGCTTTC 2580

2581 GAGCCCAAGATCCCCACAGCTCCACCGCAAGTGGTGGGCTCAACCTGCACTTCTCTC 2640  
2581 GAGCCCAAGATCCCCACAGCTCCACCGCAAGTGGTGGGCTCAACCTGCACTTCTCTC 2640  
2641 CTGGTCTTCTCTGATCTCTGGTGCATAATCGTCACTGCAATCTTGGCTCTACACGGG 2700  
2641 CTGGTCTTCTCTGATCTCTGGTGCATAATCGTCACTGCAATCTTGGCTCTACACGGG 2700  
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2701 CCTCCCTCCAGCTACAGGAACCATGAGCTGGAGGACGAGGTCTATCTTCACTCAGCTG 2760  
2761 GAGGGCTGCTCATGAGGCTGGGCTTCTCATCGGTACACCTGCTCTCTCGCGGCATC 2820  
2761 GAGGGCTGCTCATGAGGCTGGGCTTCTCATCGGTACACCTGCTCTCTCGCGGCATC 2820  
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2881 ATCACTTTCAGCATGTTGATCTTCTTCATCGTCTGATCTCTTCACTCCCGGCTATGTC 2940  
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2941 AGCACTTACGGCAAGTTTGTGCGGCGTGGAGGTGATTCGCACTCCCTGGCTCCAGCTTC 3000  
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3061 AACCACTCAGAGAGTGGCTGACGACCGGCGCCACCGCTTCAAGGTGGGCGCGG 3120  
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3121 GCCACCTCCGGCGCAGCGCGCTCTCGCAAGCGCTCCAGAGCTCTGCGGCTCCACC 3180  
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3301 ACAGGCGCATACGCCACCCCTCAGCGCACCGGCGCCGACAGGAACTCGCGGATGGCCGC 3360  
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3361 AGCGGCGACGACCTGCTTCTAGACACCAAGCGGCGCGCTCAGAAATGCGAGCCC 3420  
3361 AGCGGCGACGACCTGCTTCTAGACACCAAGCGGCGCGCTCAGAAATGCGAGCCC 3420  
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3421 CAGCGCGCAACGATGCCCGATACAAGCGGCGCGCACCAAGGCGACCTTAGAGTCCCGG 3480  
3481 GCGCGCACAGGAGCGGCCCAAACTATGAGGAAACCTTAATCCAACTCTCTCCATCAAC 3540  
3481 GCGCGCACAGGAGCGGCCCAAACTATGAGGAAACCTTAATCCAACTCTCTCCATCAAC 3540  
3541 CCCAAGAACATCTCCACGCGCAGCACCGTGCACAACTGACATCAACTCTTAAACCGGTGGC 3600  
3541 CCCAAGAACATCTCCACGCGCAGCACCGTGCACAACTGACATCAACTCTTAAACCGGTGGC 3600  
3601 TGCCCAACCTCTCCCTCTCCGCACTTTCGGTTCCTGAAAGTTCAGCATCTGAGT 3660  
3601 TGCCCAACCTCTCCCTCTCCGCACTTTCGGTTCCTGAAAGTTCAGCATCTGAGT 3660  
3661 TCCTTTTATCCTGATTTTCTGATTTTACTAGTGTGCGATATATACAAAC 3720

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Db 3661 TCCTTTATCCCTGATTTCTGACTGGATATTTACTAGTGTGCGATGGAATATCACAC 3720
Qy 3721 ATATGAGTTGCAATATAGGTGAGCAGAGTTGTGTCAAAAGTATCTGAAGT 3780
Db 3721 ATATGAGTTGCAATATAGGTGAGCAGAGTTGTGTCAAAAGTATCTGAAGT 3780
Qy 3781 ATCTGAACACTTATCTCTGAAATGTATACAAAGATTTGAAAGTATTTTACTGACA 3840
Db 3781 ATCTGAACACTTATCTCTGAAATGTATACAAAGATTTGAAAGTATTTTACTGACA 3840
Qy 3841 TTATGTTCTAAACATTTCTCAAGTAATTTGTTTACAAATAGTACCACCTGGAAGCAGT 3900
Db 3841 TTATGTTCTAAACATTTCTCAAGTAATTTGTTTACAAATAGTACCACCTGGAAGCAGT 3900
Qy 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATTAACATTTATCATTTGAAACCTGGA 3960
Db 3901 GACTGAGATTGCCACTGTGATGACAGAACTGTTTATTAACATTTATCATTTGAAACCTGGA 3960
Qy 3961 TTGCAACAGGAATATATGACTGTAAACAAAAATTTGTTGATTTATCTTAAAAATGCAAT 4020
Db 3961 TTGCAACAGGAATATATGACTGTAAACAAAAATTTGTTGATTTATCTTAAAAATGCAAT 4020
Qy 4021 TGTAATCAGATGTTAAAAATGTTAATTTCTCTGTACATTTAAATGCAATTTCTTGATA 4080
Db 4021 TGTAATCAGATGTTAAAAATGTTAATTTCTCTGTACATTTAAATGCAATTTCTTGATA 4080
Qy 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4134
Db 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4134

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RESULT 5

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US-10-270-876-17
; Sequence 17, Application US/10270876
; Publication No. US20030116096A1
; GENERAL INFORMATION:
; APPLICANT: AquaBio Product Sciences, LLC
; APPLICANT: Harris, H. William, Jr.
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous
; TITLE OF INVENTION: Fish
; FILE REFERENCE: 2213.1004-000
; CURRENT APPLICATION NUMBER: US/10/270,876
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/687,477
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Dogfish Shark
US-10-270-876-17

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Query Match 100.0%; Score 4134; DB 15; Length 4134;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 AATTCGGTTGCTGCTGCTTCAGTCCAGTCTCTCCAGTGCAAAATGAAATGTTGTC 60
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Qy 61 GCATTTACAGGAACATGCACTACATCTGTGTTAATGAAATATTTGCAATTTCTGAAGT 120
Db 61 GCATTTACAGGAACATGCACTACATCTGTGTTAATGAAATATTTGCAATTTCTGAAGT 120
Qy 121 TATTAATGTTTCTGCAAGGATGGCTTCCAGAGAAATCAATTTCTGCAAGTTTCCCAT 180
Db 121 TATTAATGTTTCTGCAAGGATGGCTTCCAGAGAAATCAATTTCTGCAAGTTTCCCAT 180

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Qy 181 GTCAATTCATGAATACTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGACCAC 240
Db 181 GTCAATTCATGAATACTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGACCAC 240
Qy 241 GTTCACCCCTTTCTTGGAGCATAGCATCAACCCCTGAAGAGATGGAAGACTTGAAGGAA 300
Db 241 GTTCACCCCTTTCTTGGAGCATAGCATCAACCCCTGAAGAGATGGAAGACTTGAAGGAA 300
Qy 301 ATGGGATTCATCTTCCAGGATTCCTGCTGAAGGATCCCTCACCATTACAAAGTAA 360
Db 301 ATGGGATTCATCTTCCAGGATTCCTGCTGAAGGATCCCTCACCATTACAAAGTAA 360
Qy 361 GCAGAAATCTCCAGGATTCCTGCTGAAGGATCCCTCACCATTACAAAGTAA 420
Db 361 GCAGAAATCTCCAGGATTCCTGCTGAAGGATCCCTCACCATTACAAAGTAA 420
Qy 421 CAGAGACAGGCTGCAAAATGGCTCAGCTTCACCTGCCAACTCTTATTTGGGATTTACA 480
Db 421 CAGAGACAGGCTGCAAAATGGCTCAGCTTCACCTGCCAACTCTTATTTGGGATTTACA 480
Qy 481 CTCCTCAGTCGTACAAATGCTCAGGATTCCTGCTGAAGGATCCCTCACCATTACAAAGTAA 540
Db 481 CTCCTCAGTCGTACAAATGCTCAGGATTCCTGCTGAAGGATCCCTCACCATTACAAAGTAA 540
Qy 541 GACATCATCTGGAGTCTCTTCCCAATACATTTGGAGTAGCCGCCAAGGATCAGGAC 600
Db 541 GACATCATCTGGAGTCTCTTCCCAATACATTTGGAGTAGCCGCCAAGGATCAGGAC 600
Qy 601 TTAATAATCGAGACCGGAGCGGACAAATGTTATTCGGTACAAATTTTCGAGCTTCCCATG 660
Db 601 TTAATAATCGAGACCGGAGCGGACAAATGTTATTCGGTACAAATTTTCGAGCTTCCCATG 660
Qy 661 CTCAGGCGATGATTTGCAATTTGAAGAGATTAACAACAGATATGATTTCTCTGCCCAAT 720
Db 661 CTCAGGCGATGATTTGCAATTTGAAGAGATTAACAACAGATATGATTTCTCTGCCCAAT 720
Qy 721 ATCACTGCGGATATGCGATATTTGACAGCTGTAAACACCGTGTCCAGGCGCTAGAGGCA 780
Db 721 ATCACTGCGGATATGCGATATTTGACAGCTGTAAACACCGTGTCCAGGCGCTAGAGGCA 780
Qy 781 ACCTCAGCTTTGTGGCCCAAGAAACAAATCGACTCGCTGAACCTTAGATGATTTCTGTAAC 840
Db 781 ACCTCAGCTTTGTGGCCCAAGAAACAAATCGACTCGCTGAACCTTAGATGATTTCTGTAAC 840
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Db 841 TGCTCTGACCATATCCCATCCAATAGCAGTGGTGGGGCAACCCGGGTGAGAAATCTCC 900
Qy 901 ACAGCTGTCGCAATCTTATTTGGGATTTATTTTACATTTCCACAGTTCAGTATGCTCTCG 960
Db 901 ACAGCTGTCGCAATCTTATTTGGGATTTATTTTACATTTCCACAGTTCAGTATGCTCTCG 960
Qy 961 AGCAGGCTGCTCAGCAACAAAGATGATCAAGGCTTCTCTGAGGACCAATCCCAATGAT 1020
Db 961 AGCAGGCTGCTCAGCAACAAAGATGATCAAGGCTTCTCTGAGGACCAATCCCAATGAT 1020
Qy 1021 GAGCAACAGGCGGCGGCGGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
Db 1021 GAGCAACAGGCGGCGGCGGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1080
Qy 1081 ACCCTGCGGCGGCGGCGGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1140
Db 1081 ACCCTGCGGCGGCGGCGGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA 1140
Qy 1141 GTTAAGAGGAGATCTGTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1200
Db 1141 GTTAAGAGGAGATCTGTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTT 1200
Qy 1201 CAGTTGAGTTTCATCGCGGAGCTTCACAGAACTCTCGGCGCAAGGTCATCTGTTGTTCTTC 1260
Db 1201 CAGTTGAGTTTCATCGCGGAGCTTCACAGAACTCTCGGCGCAAGGTCATCTGTTGTTCTTC 1260
Qy 1261 TCCAATGGCCCCGACCTGGAGCGGCTCATCCAGGAGATAGTTCCGAGAAACATCCCGAT 1320

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[illegible]

Db	2341	ACCTCCTTCGTGCTGGGGTCTTCATCAAGTTCAGAAACATCCCATCGTGAAGGCCACC	2400
Qy	2401	AACCGGAGTTGCTCACTGCTGCTCTTCTCCCTCATCTGTGCTTCTCCAGCTCGCTC	2460
Db	2401	AACCGGAGTTGCTCACTGCTGCTCTTCTCCCTCATCTGTGCTTCTCCAGCTCGCTC	2460
Qy	2461	ATCTTCATCGGCAGCCCGAGGACTGSACTGCTGCGCTCGGCCAACCGGSCTTTGGCATC	2520
Db	2461	ATCTTCATCGGCAGCCCGAGGACTGSACTGCTGCGCTCGGCCAACCGGCTTTTGGCATC	2520
Qy	2521	AGCTTCGTCTGTGCACTCTCTGCATCTCTGTGTAAGAACCAACCGGTGCTGTGCTTTC	2580
Db	2521	AGCTTCGTCTGTGCACTCTCTGCATCTCTGTGTAAGAACCAACCGGTGCTGTGCTTTC	2580
Qy	2581	GAGGCCAAGATCCCAACACAGCTTCCACCGCAAGTGGTGGGCTCAACCTGCAAGTTCCTC	2640
Db	2581	GAGGCCAAGATCCCAACACAGCTTCCACCGCAAGTGGTGGGCTCAACCTGCAAGTTCCTC	2640
Qy	2641	CTGCTCTTCTCTGCACTCTCTGTGTGCAAAATCGTCACCTGTCATCATCTGGCTCTACACCGCG	2700
Db	2641	CTGCTCTTCTCTGCACTCTCTGTGTGCAAAATCGTCACCTGTCATCATCTGGCTCTACACCGCG	2700
Qy	2701	CCTCCCTCCAGCTACAGGAAACATGAGCTTGGAGGAAGAGGTGATCTTTCATCACTGGGAC	2760
Db	2701	CCTCCCTCCAGCTACAGGAAACATGAGCTTGGAGGAAGAGGTGATCTTTCATCACTGGGAC	2760
Qy	2761	GAGGGCTCGCTCATGGCGCTGGGCTTCTCATCGGCTTACACCTGCTCTCGCGGCCATC	2820
Db	2761	GAGGGCTCGCTCATGGCGCTGGGCTTCTCATCGGCTTACACCTGCTCTCGCGGCCATC	2820
Qy	2821	TGCTTCTTCTCGCCTTCAAGTCCGTAAGCTGCGGAGAACTTCAACGAGGCTAAGTTC	2880
Db	2821	TGCTTCTTCTCGCCTTCAAGTCCGTAAGCTGCGGAGAACTTCAACGAGGCTAAGTTC	2880
Qy	2881	ATCACCTTCAGCATGTGATCTTCTTCATCGTCTGGATCTCTTTCATCCCGGCTATGTC	2940
Db	2881	ATCACCTTCAGCATGTGATCTTCTTCATCGTCTGGATCTCTTTCATCCCGGCTATGTC	2940
Qy	2941	AGCACCTACGGCAAGTTTGTGTGGCGGTGGAGGTGATTGCCATCTCTGGCTCCAGCTTC	3000
Db	2941	AGCACCTACGGCAAGTTTGTGTGGCGGTGGAGGTGATTGCCATCTCTGGCTCCAGCTTC	3000
Qy	3001	GGGTGCTGGGCTGCATTTACTTTCACAAAGTGTATCATCATCTGTTCAAGCGGTGCCGT	3060
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Qy	3061	AACACCATCGAGAGGTGCGCTGCAGCAGCGCGGCCCAACGCTTCAAGTGGGGGCCCGG	3120
Db	3061	AACACCATCGAGAGGTGCGCTGCAGCAGCGCGGCCCAACGCTTCAAGTGGGGGCCCGG	3120
Qy	3121	GCAACCTTCGGGCGCAGCGCGGCTCTCGAAGGCTTCAGAGCTGTGCGGCTCCACC	3180
Db	3121	GCAACCTTCGGGCGCAGCGCGGCTCTCGAAGGCTTCAGAGCTGTGCGGCTCCACC	3180
Qy	3181	ATCTCTCGCCGCTCGTCCACTGCGGGCCGGGCTCCACCATGGAGATGCAAGCGCTGC	3240
Db	3181	ATCTCTCGCCGCTCGTCCACTGCGGGCCGGGCTCCACCATGGAGATGCAAGCGCTGC	3240
Qy	3241	AGCACGAGAAGGTTCAGCTTTCGCGAGCGGCACCGTCACTCTGTGCTCAGCTTCGAGGAG	3300
Db	3241	AGCACGAGAAGGTTCAGCTTTCGCGAGCGGCACCGTCACTCTGTGCTCAGCTTCGAGGAG	3300
Qy	3301	ACAGGCCGATACGCCACCTTCAGCCGCAAGCGCGGAGAGGAACTCGGCGGATGGCCGC	3360
Db	3301	ACAGGCCGATACGCCACCTTCAGCCGCAAGCGCGGAGAGGAACTCGGCGGATGGCCGC	3360
Qy	3361	AGCGGCGACACCTTGCCATCTAGACACCAAGCGAGGGCCGCTCAGAAATCGAGCCC	3420
Db	3361	AGCGGCGACACCTTGCCATCTAGACACCAAGCGAGGGCCGCTCAGAAATCGAGCCC	3420
Qy	3421	CAGCCCGCACAAGATGCCGATACAGCGCGCGCCGACCAAGGCACTCTAGAGTCCGCG	3480
Db	3421	CAGCCCGCACAAGATGCCGATACAGCGCGCGCCGACCAAGGCACTCTAGAGTCCGCG	3480

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Db 3481 GCGGAGCAAGAGGCGCCCAACAATATGAGGAAACCTAATCCAACTCTCTCCATCAAC 3540
Qy 3541 CCCAAGAACATCTCCACGCGACGCGTCGACCACTGACATCAACTCTCTAACCGGTGCG 3600
Db 3541 CCCAAGAACATCTCCACGCGACGCGTCGACCACTGACATCAACTCTCTAACCGGTGCG 3600
Qy 3601 TGCCCAACCTCTCCCTCTCCGCACTTTGCGTTTGTGCGTGTGCGTGTGCGTGTGCGTGT 3660
Db 3601 TGCCCAACCTCTCCCTCTCCGCACTTTGCGTTTGTGCGTGTGCGTGTGCGTGTGCGTGT 3660
Qy 3661 TCCCTTTATCCCTGATTTCTGACTTGGATATTTACTAGTGGGATGGAATATCACAAAC 3720
Db 3661 TCCCTTTATCCCTGATTTCTGACTTGGATATTTACTAGTGGGATGGAATATCACAAAC 3720
Qy 3721 ATAAATGAGTTGCAAAATTAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACTATCTGAAGT 3780
Db 3721 ATAAATGAGTTGCAAAATTAGGTGAGCAGAGTTGTGTCAAAGTATCTGAACTATCTGAAGT 3780
Qy 3781 ATCTGAACCTATTTATCTCTCGAATTTGTTTACAAACATTTTGAAGTATTTTGTGACA 3840
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Qy 3841 TTATGTTCTAAACATTTCTCAAGATAATTTGTTTACAAATATAAGGTACCCTGAAAGCAGT 3900
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## RESULT 6

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; Sequence 7, Application US/10268051
; Publication No. US20030124090A1
; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Jury, Steven
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; APPLICANT: Linley, Timothy
; APPLICANT: Brown, Edward M.
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
; FILE REFERENCE: 2213.2004-001
; CURRENT APPLICATION NUMBER: US/10/268,051
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/328,464
; PRIOR FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
; us-10-268-051-7
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Query Match

100.0%; Score 4134; DB 15; Length 4134;

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AATTCCTGCTGTGCGTTCAGTCCAACTCTCTCCAGTCCAAATGAGAAATGGTGGTC 60
Qy 61 GCCATTACAGAACATGACATGCTGCTTAATGAATATTTGTGAGTATCTGAGGT 120
Db 61 GCCATTACAGAACATGACATGCTGCTTAATGAATATTTGTGAGTATCTGAGGT 120
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Db 121 TATTAAATATGTTTCTGCAAGGATGGCTTACAGAGAAATCAATTTCTGCACGTTTCCCAT 180
Qy 181 GTCAATGTATGAAATACTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGCCAC 240
Db 181 GTCAATGTATGAAATACTGACCAAGGATGTAAACAAATGGAACAAAGCTGAGGCCAC 240
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Qy 301 ATGGGATGATCTTCCAGGATTTCTGTAAAGCGATCCCTCACCATTAACAAATAA 360
Db 301 ATGGGATGATCTTCCAGGATTTCTGTAAAGCGATCCCTCACCATTAACAAATAA 360
Qy 361 GCAGAAATCTCTCAGGATCTCTGTAAACGGCTGCGTAGTGTGGTTCAGAGGAA 420
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Db 421 CAGAGACAGGGCTGCACAAATGGCTCAGCTTCACTGCCAACTTTATTTCTGGGATTTACA 480
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Db 481 CTCCTCAGTCTGACATGCTCAGGGTATGGTCCAAACAAAGGGCCAGAGAAAGGA 540
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Db 541 GACATCATATGCGGAGGTCTCTTCCCAATACACTTTGGAGTAGCCGCCAAGGATCAGGAC 600
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Qy 661 CTCAGGCGGATGATTTTCGCAATTTGAAGATTAACAAAGTATGACTTTCTTCCGCCAAT 720
Db 661 CTCAGGCGGATGATTTTCGCAATTTGAAGATTAACAAAGTATGACTTTCTTCCGCCAAT 720
Qy 721 ATCACTCTGGGATATGCAATATTTGACAGCTGTAAACACCGTGTCCAGGCGCTAGAGGCA 780
Db 721 ATCACTCTGGGATATGCAATATTTGACAGCTGTAAACACCGTGTCCAGGCGCTAGAGGCA 780
Qy 781 ACACCTCAGCTTTGTGGCCAGAACAAATCGACTCTCTGAACTTAGATGATGTTCTGTAAAC 840
Db 781 ACACCTCAGCTTTGTGGCCAGAACAAATCGACTCTCTGAACTTAGATGATGTTCTGTAAAC 840
Qy 841 TGCTCTGACCATATCCCATCCACAATAGCAGTGTGGGCGCAACCGGGTCAGGAATCTCC 900
Db 841 TGCTCTGACCATATCCCATCCACAATAGCAGTGTGGGCGCAACCGGGTCAGGAATCTCC 900
Qy 901 ACGCTGTGCGCAATCTATTTGGGATTTATTTACATTTCCACAGTTCAGCTATGCTCTCTCG 960
Db 901 ACGCTGTGCGCAATCTATTTGGGATTTATTTACATTTCCACAGTTCAGCTATGCTCTCTCG 960
Qy 961 AGCAGGCTGCTCAGCAACAAAGATGATCAAGGCTTCTCTGAGGACCATCCCAATGAT 1020
Db 961 AGCAGGCTGCTCAGCAACAAAGATGATCAAGGCTTCTCTGAGGACCATCCCAATGAT 1020
Qy 1021 GAGCAACAGGCGCAGCGCATGGCGAGATCATCGAGACTTCCAGTGGAACTGGGTGGGA 1080
Db 1021 GAGCAACAGGCGCAGCGCATGGCGAGATCATCGAGACTTCCAGTGGAACTGGGTGGGA 1080
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Qy 3241 AGACGCGAAGGTGAGTCTGCGCAGCGGACCGTCAACCTGTCGCTCAGCTTCGAGGAG 3300
Db 3241 AGACGCGAAGGTGAGTCTGCGCAGCGGACCGTCAACCTGTCGCTCAGCTTCGAGGAG 3300
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Db 3301 ACAGGCGGATACCGCCACCTCAGCCGACGGCCGCGAGGAGGAGTCCGCGATGCGCGC 3360
Qy 3361 AGCGGCGAGACCTGCGCATCTAGACACCGACCGGCGCGCTCAGAAATGCGAGGCC 3420
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Db 4021 TGTAAATCAGATGTGTAATTTGTAATTTCTGTACATAAATGCAATTTCTTTGATA 4080
Qy 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCCCGCAGCAACGG 4134
Db 4081 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCGCCCGCAGCAACGG 4134

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RESULT 7

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US-10-125-772-1
; Sequence 1, Application US/10125772
; Publication No. US20030124657A1
; GENERAL INFORMATION:
; APPLICANT: MariCal
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-006
; CURRENT APPLICATION NUMBER: US/10/125,772

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; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Squalus acanthias
US-10-125-772-1

Query Match
Best Local Similarity 100.0%; Score 4134; DB 15; Length 4134;
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTCCGTTGTCGCTTCCAGTCCCAAGTCTCTCCAGTCCAAATGAGAAATGTTGGTTC 60
Db 1 AATTCCGTTGTCGCTTCCAGTCCCAAGTCTCTCCAGTCCAAATGAGAAATGTTGGTTC 60
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Qy 4021 TGTAAATCAGATGTGTAATTTGGTAATTAATCTCTGTACATTAATTAATTTCTTGATA 4080  
Db 4021 TGTAAATCAGATGTGTAATTTGGTAATTAATCTCTGTACATTAATTAATTTCTTGATA 4080

Qy 4081 AAGCGGCCGACAGCAACGG 4134  
Db 4081 AAGCGGCCGACAGCAACGG 4134

## RESULT 8

US-10-016-496-1  
; Sequence 1, Application US/10016496  
; Publication No. US20030166908A1  
; GENERAL INFORMATION:  
; APPLICANT: H. William Harris  
; APPLICANT: Edward M. Brown  
; APPLICANT: Steven C. Hebert  
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic  
; FILE REFERENCE: 2856.1001-007  
; CURRENT APPLICATION NUMBER: US/10/016,496  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: US/09/162,021B  
; PRIOR FILING DATE: 1998-09-28  
; PRIOR APPLICATION NUMBER: PCT/US97/05031  
; PRIOR FILING DATE: 1997-03-27  
; PRIOR APPLICATION NUMBER: 08/622,738  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 4134  
; TYPE: DNA  
; ORGANISM: squalus acanthias  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (439)...(3522)  
US-10-016-496-1

Query Match 100.0%; Score 4134; DB 15; Length 4134;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 481 CTCCTACAGTCGTACATATGTTCTCAGGGTATGTTCTCCAAACCAAGAGGCCCAAGAGGA 540

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541	QY	GACATCATCTGAGGAGTCTCTTCCCAATACACTTTGAGTAGCGCCAAAGGATCAGGAC	600
541	DB	GACATCATCTGAGGAGTCTCTTCCCAATACACTTTGAGTAGCGCCCAAGGATCAGGAC	600
601	QY	TTAAATCGAGACCGGAGGCGACAAAATGTATTCCGTACAATTTTCGAGGCTTCCGATGG	660
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661	QY	CTCCAGGGGATGATTTCCGAATTCAGAGATTAACAACAGTATGACTTTCTTCGCCCAAT	720
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781	DB	ACACTCAGCTTTGTGGCCCGAGAACAAATCGACTCGCTGAACCTTAGATGAGTCTGTAAAC	840
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841	DB	TGCTCTGACCATATCCCATCCAAATAGCAGTGTGCGGGCAACCGGGTCAGGAATCTCC	900
901	QY	ACGGCTGTGGCAATCTATTGGGATTTATTTACATTCACAGTCACTATGCTCTCTCG	960
901	DB	ACGGCTGTGGCAATCTATTGGGATTTATTTACATTCACAGTCACTATGCTCTCTCTCG	960
961	QY	AGCAGGCTGCTCAGCAACAAGAAATGAGTACAAGGCCCTTCCTGAGGACCATCCCCCAATGAT	1020
961	DB	AGCAGGCTGCTCAGCAACAAGAAATGAGTACAAGGCCCTTCCTGAGGACCATCCCCCAATGAT	1020
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1021	DB	GAGCAACAGGCCACGGCCATCGCCGAGATCATCGAGCACTTCCAGTGGAACTGGGTGGGA	1080
1081	QY	ACCTTGGCAGCGCAGTAGACTATGCGCGCCACAGGCATTGACAAGTTCCCGGAGGAGGCC	1140
1081	DB	ACCTTGGCAGCGCAGTAGACTATGCGCGCCACAGGCATTGACAAGTTCCCGGAGGAGGCC	1140
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1141	DB	GTTAAGAGGGACATCTGTPATTGACTTCAGTGGAGATGATCTCTCAGTACTACACCAGAAG	1200
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1201	DB	CAGTTGGAGTTCACTGCCGACGTATCCAGAACTCTCTCGGCCAAGGTATCGTGGTCTTC	1260
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1261	DB	TCCAAATGCCCCGACCTGGAGCGCTCATCCAGGAGATAGTTCCGAGGAAACATCACCCGAT	1320
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1321	DB	CGGATCTGGCTGGCCAGCGAGGCTTTGGCCAGCTCTTCGCTCATTTGCCAAGCAGAGTAC	1380
1381	QY	TTCCACGTGTGGCGGCACCATCGGCTTCCTCAGGGCGGGCGTATCCCAAGGTTTC	1440
1381	DB	TTCCACGTGTGGCGGCACCATCGGCTTCCTCAGGGCGGGCGTATCCCAAGGTTTC	1440
1441	QY	AACAAGTTCTGAAGGAGGTCCACCCAGCAGGTCCTTCGGAATATGGTTTGTCAAGAG	1500
1441	DB	AACAAGTTCTGAAGGAGGTCCACCCAGCAGGTCCTTCGGAATATGGTTTGTCAAGAG	1500
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1501	DB	TTCTGGGAGGAGACTTCAACTGCTACTTACCCGAGAGACCTTCGACGACTCAAGAAT	1560
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Db	1561	TCCAAGGTGCCCTCGCACGGACCGGGCGGTCAAGGGGA	CGGCTTCAAGGGCGGGGAACCTCC	1620
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Qy	1681	CCCTACCTGGATTATACACACCTTGAGATCTCTCAAAATGTATACGTGGCCGCTACTCC		1740
Db	1681	CCCTACCTGGATTATACACACCTTGAGATCTCTCAAAATGTATACGTGGCCGCTACTCC		1740
Qy	1741	ATTGCTCAGCCCTGCAAGACATCCACTCTTGCAAAACCCGGCACGGGCATCTTTGCAAAAC		1800
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Qy	1801	GGATCTTTGGCAGATATATAAAAGTTGAGGCTGGCAGGTCTCTCAACATCTGCTGCAT		1860
Db	1801	GGATCTTTGGCAGATATATAAAAGTTGAGGCTGGCAGGTCTCTCAACATCTGCTGCAT		1860
Qy	1861	CTGAAGTTTACCACAGCATGGGTGACAGTTTGACTTTGACCATCAAGGTGACCTCAAG		1920
Db	1861	CTGAAGTTTACCACAGCATGGGTGACAGTTTGACTTTGACCATCAAGGTGACCTCAAG		1920
Qy	1921	GGGAACTPACACCATTAACAATGGCAGCTCTCCGACAGAGATGAATCGGTGTTTCCAT		1980
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Qy	1981	GAGGTGGCAACTACRAACGCTACGCTTAAGCCAGTGACCGACTCAACATCAACGAAAG		2040
Db	1981	GAGGTGGCAACTACRAACGCTACGCTTAAGCCAGTGACCGACTCAACATCAACGAAAG		2040
Qy	2041	AAAACTCTCGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTSCAGTCGAGACTGT		2100
Db	2041	AAAACTCTCGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTSCAGTCGAGACTGT		2100
Qy	2101	GTCCGGGCACAGGAAGGGGATCATCGAGGGGAGCCCACTGCTGCTTTGAATGCATG		2160
Db	2101	GTCCGGGCACAGGAAGGGGATCATCGAGGGGAGCCCACTGCTGCTTTGAATGCATG		2160
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Qy	2221	AATGATTTCTGTCGAATGAGAACCAACAGTCTGTGCATCGCCAGAGAGATCGAGTACTG		2280
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Qy	2281	TCGTGGAAGGAGCCCTTCGGGATCGCTGCACCATCTTCGCCGTACTGGGCATCTCTGATC		2340
Db	2281	TCGTGGAAGGAGCCCTTCGGGATCGCTGCACCATCTTCGCCGTACTGGGCATCTCTGATC		2340
Qy	2341	ACCTCCTTCGTGTCGGGGTCTTCAATCAAGTTGAGGAACAATCCCATCTGTGAAGGCCACC		2400
Db	2341	ACCTCCTTCGTGTCGGGGTCTTCAATCAAGTTGAGGAACAATCCCATCTGTGAAGGCCACC		2400
Qy	2401	AACCGGAGTTGCTTACCTACCTGCTCTTCTCCTCATCTGCTTCTCCAGCTCGCTC		2460
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Qy	2461	ATCTTCATTCGGCGAGCCCGAGACTGACCTGTGGCTCCGCCAAACCGGCCCTTTGGCATC		2520
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Qy	2521	AGCTTCGTCTGTGCATCTCTGCATCTCGTGAAGACCAACCGGGTGTCTGCTCTTC		2580
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Qy	2581	GAGGCCAAGATCCCAACAGCCTCCACCGCAAGTGGGTGGGCCCTCAACCTGCAGTTCTTC		2640
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Qy	2641	CTGCTCTTCTCTGCATCTGGTGCAAAATGTCACCTGTCATCTCTGGCTCTACACCGG		2700
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QY 301 ATGGGGATTGATCTTCCAGGAGTTCGTGTAAAGGATCCCTCACCAATTACAAAGATAA 360  
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RESULT 10  
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; Sequence 17, Application US/10410872  
; Publication No. US20030230247A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, H. William, Jr.  
; APPLICANT: Russell, David R.  
; APPLICANT: Nearing, Jacqueline  
; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Methods for Raising Pre-Adult Anadromous  
; FILE REFERENCE: 2213.1004-001  
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; CURRENT FILING DATE: 2003-04-09  
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; PRIOR FILING DATE: 2001-10-11  
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; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 09/687,476  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 09/687,372  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 4134  
; TYPE: DNA  
; ORGANISM: Dogfish Shark  
US-10-410-872-17

Query Match 100.0%; Score 4134; DB 15; Length 4134;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;







<p>                     ; PRIOR FILING DATE: 2002-04-18                      ; PRIOR APPLICATION NUMBER: 10/125,792                      ; PRIOR FILING DATE: 2002-04-18                      ; PRIOR APPLICATION NUMBER: 10/121,441                      ; PRIOR FILING DATE: 2002-04-11                      ; PRIOR APPLICATION NUMBER: PCT/US01/31704                      ; PRIOR FILING DATE: 2001-10-11                      ; PRIOR APPLICATION NUMBER: 60/240,392                      ; PRIOR FILING DATE: 2000-10-12                      ; PRIOR APPLICATION NUMBER: 60/240,003                      ; PRIOR FILING DATE: 2000-10-12                      ; NUMBER OF SEQ ID NOS: 40                      ; SOFTWARE: PatentIn version 3.2                      ; SEQ ID NO 1                      ; LENGTH: 4134                      ; TYPE: DNA                      ; ORGANISM: Squalus acanthias                      ; US-10-410-885-1                 </p>		<p>                     Query Match 100.0%; Score 4134; DB 15; Length 4134;                      Best Local Similarity 100.0%; Pred. No. 0;                      Matches 4134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                 </p>	
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3601 TGCCCAACCTCTCCCTCTCGGCGACTTTGCGTTTGTGGAAGATTGCGAGCTCTGAGT 3660  
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3661 TCCCTTTATCCCTGATTTCTGACTTGGATTTTACTAGTGTGCGATGGAATATCAAC 3720  
3661 TCCCTTTATCCCTGATTTCTGACTTGGATTTTACTAGTGTGCGATGGAATATCAAC 3720  
3721 ATAATGAGTTCACAATTAGGTGAGCAGATTGTGTCAAAAGTATCTGAATCTCTGAAGT 3780  
3721 ATAATGAGTTCACAATTAGGTGAGCAGATTGTGTCAAAAGTATCTGAATCTCTGAAGT 3780  
3781 ATCTGACTACTTATCTCTCGAATTTGATTAACAACATTTTGAAGTATTTTAGTGACA 3840  
3781 ATCTGACTACTTATCTCTCGAATTTGATTAACAACATTTTGAAGTATTTTAGTGACA 3840  
3841 TTAATGTTCTAACAATTTGCAAGATAAATTTGTTTCAACATATAAGGTACCACCTCAAG 3900  
3841 TTAATGTTCTAACAATTTGCAAGATAAATTTGTTTCAACATATAAGGTACCACCTCAAG 3900  
3901 GACTGAGATTGCCACTGTGTGATGACAGACTGTTTTTATTAACATTTTCAATGAACTGGA 3960  
3901 GACTGAGATTGCCACTGTGTGATGACAGACTGTTTTTATTAACATTTTCAATGAACTGGA 3960  
3961 TTGCAACAGGAATATTAATGACTGTAAACAAAAAATTTGTTGATTTATCTTAAAAATGCAA 4020  
3961 TTGCAACAGGAATATTAATGACTGTAAACAAAAAATTTGTTGATTTATCTTAAAAATGCAA 4020  
4021 TGTAAATCAGATGTGTAAATTTGTTAATTAATCTCTGTACATTAATGATATTTCTTGATA 4080

Db	4021	TGTAATCAGATGTAATAATCGTAATTAATCTCTGTACATTAATAATGCAATTTCTTGATA	4080
Qy	4081	AAGCGCCGACAGCAACGG	4134
Db	4081	AAGCGCCGACAGCAACGG	4134
RESULT 12			
US-10-225-567A-117			
; Sequence 117, Application US/10225567A			
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; GENERAL INFORMATION:			
; APPLICANT: Lifespan Biosciences			
; APPLICANT: Brown, Joseph P.			
; APPLICANT: Burmer, Glenna C.			
; APPLICANT: Roush, Christine L.			
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS			
; FILE REFERENCE: 1920-4-4			
; CURRENT APPLICATION NUMBER: US/10/225,567A			
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; NUMBER OF SEQ ID NOS: 2292			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 117			
; LENGTH: 3783			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-225-567A-117			
Query Match 42.2%; Score 1745.2; DB 15; Length 3783;			
Best Local Similarity 76.4%; Pred. No. 0;			
Matches 2187; Conservative 0; Mismatches 658; Indels 17; Gaps 3;			
Qy	501	CTCAGGGTATGGTCCAAACCAAGGGCCGAGAGAAAGAGAGACATCATCTGGGAGGCT	560
Db	423	CTCTGCTCCTAGCGCCAGAGCCAGGAGCCCAAGAGAGGGGACATTTATCTTTGGGGGCT	482
Qy	561	CTTCCCAATACATTTGGAGTAGCCGCAAGNATCAGACTTAATAATCGAGCCGAGGC	620
Db	483	CTTTCCTATTCAATTTGGAGTAGCAGCTAAGATCAAGATCTCAAACTGAAGCCCGGAGTC	542
Qy	621	GACAAATGATTCGGTCAAAATTTTCGAGGCTTCCGATGGCTCCAGCGGATGATTCGC	680
Db	543	TGTGGATGATCAGGTAATAATTCGTTGGGTTTCGTTGTTACAGGCTATGATATTGC	602
Qy	681	AATTGAAGATTAACAAGATGATCTTCTTCCGCCAATATCACCCCTGGGATATCGCAT	740
Db	603	CATAGAGGATATAACAGCAGCCAGCCCTTCTTCCCAACTTGACGCTGGGATACAGGAT	662
Qy	741	ATTTGACAGGTAAACACCGGTGTCAGGCGCTAGAGGCAACACTCAGCTTTGTGGCCCA	800
Db	663	ATTTGACACTTGCAACACCGTTTCTAAGGCTTTGGAAGCCACCCTGAGTTTGTGCTCA	722
Qy	801	GAACAAATCGACTCGCTGAACCTAGATGAGTTCTGTAACTGTCTGACCATATCCATC	860
Db	723	AAACAAATGATTTCTTTGAACCTTGATGAGTTCTGCAACTGTCTGAGACATATCCCTC	782
Qy	861	CACATAGAGTGTGGGGCAACCGGTGAGGAATCTCCAGCGCTGCGCCAACTATT	920
Db	783	TAGGATTTGCTGTGGTGGGACCACTGGCTCAGGCGTCTCCAGCGAGTGGCAATCTGCT	842
Qy	921	GGGATTAATTTACATTCACAGGTCACTATGCTCTCTCTCGAGCAGGCTGCTCAGCAACA	980
Db	843	GGGGCTCTTCTACATTCCTCCAGGTCACTATGCTCTCTCTCGAGCAGACTCTCTCAGCAACA	902
Qy	981	GAATGAGTACAGGCTTCTGAGGACCATCCCAATGATGACCAACAGCCACGCCAT	1040
Db	903	GAATCAATTAAGTCTTTCTCCGAAACCAATCCCAATGATGACCAACAGGCTCTCCAT	962
Qy	1041	GGCGAGATCATCGAGCACTTCCAGTGAACCTGGTGGAACTGGTGGAACTGGTGGAGTGTCTGATGGGAGTA	1100

Db	963	GGCAGACATCATCAGATTAATTTTCGCTGGAACCTGGTGGGCACAAATTCAGCTGATGACGA	1022
Qy	1101	CTATGGCCGCCAGGCAATGACAAGTTCCGGGAGGAGCGCGTTAAAGAGGACATCTCTAT	1160
Db	1023	CTATGGCGGCGGGGATTCAGAAATTCGAGAGGAAGCTGAGGAAAGGATATCTGTCAT	1082
Qy	1161	TGACTTCAGTGCAGATGATCTCTCAGTACTACCCAGAACAGTTGGAGTTCTATCGCCGA	1220
Db	1083	CGACTTCAGTGAATCATCTCCAGTACTCTGTATGAGGAAGATCCAGCATGTGTAGA	1142
Qy	1221	CGTCATCCAGAACTCTCGGCCAAGGTCATCGTGGTCTTCTCCAAATGGCCCGACCTGGA	1280
Db	1143	GGTGATTCAAATTCACAGGCCAAAGTCATCGTGGTCTTCTCCAGTGGCCAGATCTTGA	1202
Qy	1281	GCCGCTCATCCAGAGATAGTTCCGAGAAACATCACCGATCGGATCTGGTGGCCACCGA	1340
Db	1203	GCCCTCATCAAGAGATGTCGCGGCAATATCACGGCAAGATCTGGTGGCCACCGA	1262
Qy	1341	GGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCCAGAGTACTTCCACGTGGTCCGCGCAC	1400
Db	1263	GGCTTGGCCAGCTCTCTCCCTGATCGCATGCTCAGTACTTCCACGTGGTGGCGCAC	1322
Qy	1401	CATCGGCTTCGCTCTCAGGGCGGGCGTATCCGAGGTTCAACAGTTCTCTGAAGAGGT	1460
Db	1323	CATTGGATTCGCTCTGAAGGCTGGGCAGATCCCAAGGCTTCGGGAAATTCCTGAAGAAGT	1382
Qy	1461	CCACCCAGCAGGTCCTCGGACATGGTTCGTCAGAGGTTCTGGGAGGAGACCTTCAA	1520
Db	1383	CCATCCAGAGAGTCTGTCCAAATGTTTTCGCAAGAGTTTGGGAAGAAACATTTAA	1442
Qy	1521	CTGCTACTTCAACGAGAAGACCTTCAGCAGCTGAAGAAATTCGAAGTGGCCCTCGCAGG	1580
Db	1443	CTGCCACCTCCAAGA-----AGGTGCAAAAGGACCTTTACCTGTGGACACCTTTCTG	1494
Qy	1581	ACCGCGGCTCAAGGGGACCGCTCCAGGGGGGAACTCCAGAGGAGAGCCCTTACGCCA	1640
Db	1495	AGAGG----TCACGAAGAAAGTGGCGACAGTTTAGCAACAGCTCGACAGCTTCCGACC	1550
Qy	1641	CCCCTGCACTGGGAGAGAGAACATCACAGCGTGGAGACCCCTTACCTGGATTATACACA	1700
Db	1551	CCTCTGTACAGGGATGAGAACATCAGCAGTGTGAGACCCCTTACATAGATTACAGCA	1610
Qy	1701	CCTGAGGATCTCTCAATGATAGTGGCGGCTCTCTCCATTTGCTCAGCCCTTGCAGA	1760
Db	1611	TTTACGATATCTTCAATGTGTACTTAGCAGTCTACTCCATTCGCCAGCTTGCAGA	1670
Qy	1761	CATCCACTTTGCAAAACCCGSCACGGCATCTTTGCAAAACGGATCTTGTGCAGATATTAA	1820
Db	1671	TATATATACCTCTTACTCTGGAGAGGGCTCTTCCAAATGGCTCTCTGTGCAGACATCA	1730
Qy	1821	AAAAAGTTAGGCTTGGCAGGTCCTCAACCATCTGCTGCACTGAAGTTTACCAACAGAT	1880
Db	1731	GAAAGTTGAGCGTGGCAGGTCCTGAAGCACCTACGGCATCTAAACITTTACAAACAATAT	1790
Qy	1881	GGGTGAGCAGGTTGACTTTGACGATCAAGGTGACCTCAAGGGGAACCTACACATTATCAA	1940
Db	1791	GGGGAGCAGGTGACCTTTGATGAGTGTGGTGAACCTGGTGGGGAACCTATTCATCATCA	1850
Qy	1941	CTGGCAGCTCTCCGACAGAGTGAATCGGTGTTTCTTCCATGAGTGGGCAACTACAACGC	2000
Db	1851	CTGGCACCTCTCCGACAGAGTGGCTCCATCGTGTGTTAAGGAAGTTCGGGTATTACAAGT	1910
Qy	2001	CTACGCTAAGCCCGAGTGAACGACTCAACATCAACGAAAGAAATCTCTGGAGTGGCTT	2060
Db	1911	CTATGCCAAGAGGAGGAGAAAGACTCTTCATCAACGAGAGAAATCTCTGGAGTGGGTT	1970
Qy	2061	CTCCAAAGTGGTCTCTTCTCCAACTGCACTGAGAGTGTGTGCGGGGACACAGGAAGGG	2120
Db	1971	CTCCAGGAGGTTGCTCTCTCCAACTGCACTGAGAGTGTGCTTGGCAGGGACAGGAAGG	2030
Qy	2121	GATCATCAGGGGAGGCCACCTGCTGTTTGAATGATGCAATGTCATGTGCAGAGGAGGTT	2180
Db	2031	GATCATTCAGGGGAGGCCACCTGCTGTTTGAATGATGTCATGTGAGTGTCTGATGGGAGTA	2090







591	Db	GGCAGACATCATCGAGTATTTCGGCTGGAACTCGGGTGGGCACAATTTGCAGCTCATGACGA	650
1101	Qy	CTATGGCCGCCACAGGCATTCACAAGTTCCGGGAGGAGCGGTTTAAAGAGGACATCTGTAT	1160
651	Db	CTATGGCCGCCCGGGATTGGAATTTCCGAGAGGAAGCTTGAGAAAGGATATCTGCAT	710
1161	Qy	TGACTTCAGTGAATGATCTCTCAGTACTACTACCCAGAAACAGTTGGAGTTCAATCGCCGA	1220
711	Db	CGACTTCAGTGAATCATCTCTCCAGTACTCTGATAGGAAGAGATTCAGCATGTGATAGA	770
1221	Qy	CGTCATCCGAATCTCTCGGCCAAGTCATCGTGTCTTCTCCAAATGGCCCCACCTGGA	1280
771	Db	GGTGATTCAAAATTCACGGCCAAAGTCACTGGTGGTTTCTCCAGTGGCCCCAGATCTTGA	830
1281	Qy	GCCTCATCCAGAGATAGTTTCGGAGAAACATCACCGATCGGATCTGGCTGGCCACGCGA	1340
831	Db	GCCCTCATCAAGAGATGTCGCGGCCAATATACGGGGCAAGATCTGGCTGGCCACGCGA	890
1341	Qy	GGCTTGGCCAGCTCTTCGCTCATTTGCCAAGCAGAGTACTTCCAGTGTGCGCGGCAC	1400
891	Db	GGCTGGCCAGCTCTCTCCCTGATTCGGCATGCGCTACTTCCAGTGTGCGCGGCAC	950
1401	Qy	CATCGGCTTCGCTCTCAGGGCGGGCGTATCCCAAGGTTTCAACAAGTTCTCTGAAGAGGT	1460
951	Db	CATTGATTCGCTCTGAAGCTGGGCAGATCCACAGCTTCGGGAATTCCTGAAGAAGT	1010
1461	Qy	CCACCCAGCAGGTCTCTGGACAAATGGTTTGTCAAGGATTTCTGGAGGAGACCTTCAA	1520
1011	Db	CCATCCAGGAAGTCTCTCCACAATGGTTTTCACAAGAGTTTTCGGAAGAAACATTTAA	1070
1521	Qy	CTGCTACTTCACCGAGAAGACCCCTGACGCGAGCTGAAGAAATCCAAGTGCCTCGCACGG	1580
1071	Db	CTGCCACTTCAAGA-----AGTGTCAAAGGACCTTTACTGTGGACACTTCTCTG	1122
1581	Qy	ACCGCGGCTCAAGGGACCGCTCCAAAGCGGGGAATCCAGACGGACAGCCCTACGCCA	1640
1123	Db	AGAGG----TCAGAGAAAGTGGCGACAGGTTTAGCAAAGCTCGACAGCCTTCGAGCC	1178
1641	Qy	CCCTGCACCTGGGAGAGACATCACAGGTTGGAGACCCCTTACTGTGATTTATACACA	1700
1179	Db	CCTCTGTACAGGGGATGAGAAATCAGCAGTGTGAGACCCCTTACATGATTACACGCA	1238
1701	Qy	CCTGAGGATCTCTTACAATGTATACGTGGCGCTTACTCCTCATTTGCTCACGCCCTGCAAGA	1760
1239	Db	TTTACGGATATCTTACAATGTGTACTTAGCAGTCTACTCCTATTGCCACGCCTTGCAAGA	1298
1761	Qy	CATCCACTTTGMAAACCGGACAGGGCATCTTTGAAAACGATCTTTGCGAGATTTAA	1820
1299	Db	TATATATACCTGTACTCTGGAGAGGGCTCTTCACCAATGGCTCTGTGCGACATCAA	1358
1821	Qy	AAAAGTTGAGCCTGGCAGGTCCTCAACCATCTGCTGCATCTGAAGTTTACCAACAGCAT	1880
1359	Db	GAAAGTTGAGCGTGGCAGGTCCTGAGACCTTACGGCATCTAACTTTACAAACATAT	1418
1881	Qy	GGGTGACAGGTTGACTTTGACGATCAAGGTGACCTCAAAGGGAATCTACACCATTTCAA	1940
1419	Db	GGGGACAGGTGACCTTTGATAGTGTGGTGACCTGGTGGGAACTATTTCATCATCAA	1478
1941	Qy	CTGGAGCTCTCCGACAGGATGAATCGGTGTCTTCCATGAGTGGCGCACTACACGC	2000
1479	Db	CTGGCACTCTCCCCAGAGGATGGCTCCATCGTGTTTAAGGAAGTCGGGTATTACAACT	1538
2001	Qy	CTACGCTAAGCCCACTGACCGACTCAACATCAAAGAAAGAAATCTCTGGAGTGGCTT	2060
1539	Db	CTATGCCAAGAGGAGAAAGACTCTTCATCAACAGGAGAAATCTGTGGAGTGGTTT	1598
2061	Qy	CTCAAAGTGGTTCTTTCTCCAACTGCAGTCTGAGACTGTGTCGGGGCACCGAGAGGG	2120
1599	Db	CTCCAGGAGGTGCCCCCTTCTCCAACTGCAGCCGAGACTGGCTTGCAGGGAACGAGAAAG	1658
2121	Qy	GATCATCGAGGGGAGGCCACTCTGCTGTGTTGAATGCAATGTCATGTCTCAGAGGAGAGTT	2180

Db	1659	GATCA	TTGAGGGGGAGCCACCTGCTGTTTGAGTGTGTGGAGTGTCTGATGGGGAGTA	1718				
Qy	2181	CAGTGA	TGAAACCGATGCAAGTCCGTGTGA	CAAAGTGC	CCGAATATTTCTCGT	CGAAATGA	2240	
Ds	1719	TAGTGA	TGAGACAGATGCCAGTGCCTGTAA	CAAAGTGCC	AGATGACTTCTGGT	CCAATGA	1778	
Qy	2241	GAACCA	ACACGTGATGATCGCAAGGAGATCGAGTAC	TCTGTCTG	TGGA	CGGAGCCCTTCGG	2300	
Ds	1779	GAACCA	CAACCTCTGATTTGCCAAGGAGATCGAGTTT	CTGTCTG	TGGA	CGGAGCCCTTCGG	1838	
Qy	2301	GATCGCT	CTTGACCATCTTCGCGCGTACTGGGCATCCTGAT	CACCTCTCT	CGTGC	TGGGGGT	2360	
Ds	1839	GATCGCACT	CACCCCTTTTTCGCGTCTGGGCATTTTCTCTG	ACAGCC	TTTGTGCT	TGGGTGT	1898	
Qy	2361	CTTTCAT	CAAGTTGAGAAACATCTCCCATCGTGAAGGCC	ACCAACCGG	AGTTGTCT	TACCT	2420	
Ds	1899	GTTTAT	CAAGTTCCGCAACACACCACTATGTCAAGGCC	ACCAACCGG	AGTCTCT	CTCTACCT	1958	
Qy	2421	GCNTGCT	CTTCTCCATCTGCTGCTCTTCAGAGTCTGCTCAT	CTTCTATCG	CGGAGCCACG		2480	
Ds	1959	CTTCTCT	CTTCTCTGCTCTGCTGCTTTCTTCAGAGTCTCCCTGTT	CTTTCAT	CGGAGCCGCA		2018	
Qy	2481	GGACTG	GAACCTGTCGCTCCGC	CAACCGG	CCCTTTGGCATCAAGTTCGTC	TGTGCATCTC	2540	
Ds	2019	GGACTG	GAACCTGTCGCTCCGC	CAGCGG	CCCTTTGGCATCAAGTTCGTC	TGTGCATCTC	2078	
Qy	2541	CTGCAT	CTCTGGTGAAGACAAACCGGGTCTGCTGCTCTTCG	AGGCCAAGATCC	CCACACG		2600	
Ds	2079	ATGCAT	CTCTGGTGAAGAACAAACCGTCTCTCTGCTGTTG	AGGCCAAGATCC	CCACACG		2138	
Qy	2601	CTTCCAC	CGCAAGTGGTGGGGCTCAACCTG	CAGTTCCTCTG	TCGTCCTCTGCATCCT		2660	
Ds	2139	CTTCCAC	CGCAAGTGGTGGGGCTCAACCTG	CAGTTCCTCTG	TCGTCCTCTGCATCCT		2198	
Qy	2661	GGTGCA	AAATGCTCACCTGATCATCTG	TGGCTTACACCGG	GCCTCCCTCGAGTACAGAA		2720	
Ds	2199	CATGCA	GTATCTGTTGATCTGGCTCTACACCG	CGGCCCTCAAGCT	ACCGCAA		2258	
Qy	2721	CCATGAG	CTGGAGCAGAGTCACTTTCACT	CACCTGCGACGAGG	CTCGCTCATGGCGCT		2780	
Ds	2259	CCAGGAG	CTGGAGATGAGATCATCTTCA	TACAGTGCACGAGG	GCCTCCCTCATGGCCCT		2318	
Qy	2781	GGGCTT	CTCTCATCGGTTACACTGCTCTCTCGCG	CCATCTGCTTCTTCT	TCGCCCTTCAA		2840	
Ds	2319	GGGCTT	CTCTCATCGGTTACACTGCTCTCTCGCG	CCATCTGCTTCTTCTT	CGCTTCAA		2378	
Qy	2841	GTCCGT	TAAGTCCCGGAGAACTTCAA	CAGAGCTAAGTTTCAT	CACCTTCAGATGTTGAT		2900	
Ds	2379	GTCCGG	AAGCTGCCGGAGAACTTCA	TGAGC	CAAGTTTCATC	ACTTCAGCATGCTCAT	2438	
Qy	2901	CTTCTT	CATGCTGTGATCTCTTCATCC	CGCCCTATGTCAG	CACTACGGCAAGTTTGT		2960	
Ds	2439	CTTCTT	CATGCTGTGATCTCTTCATTC	ACGCTTATGCGAG	CACTATGGCAAGTTTGT		2498	
Qy	2961	GTGGCG	GTGGAGTCAATGTCATCTTGCCATCCTG	GCCTTCAGCTTCGG	CTCTGGCTGCATTTA		3020	
Ds	2499	CTTGC	CGTATAGGTTATGTCATCTCTG	CAGCCAGCTTTGGCTT	GTCTGGCGTGTGATCTT		2558	
Qy	3021	CTTCA	CAAGTGTTCATCATCTGT	TCAAAGCCGTGCGGTAA	CACTACGAGGAGTGC		3080	
Ds	2559	CTTCA	CAAGATCTACATCATCTT	CAAGCCATCCCGCA	ACCATCGAGGAGTGC		2618	
Qy	3081	CTG	CAGCA	CGGCGGCCACGCCTT	TAAGTGTGGCGCGGGCC	ACCCTTCGGCGGAGGC	3140	
Ds	2619	TTG	CAGCA	CGCAGCTC	ACGCTTTCAAGTGTG	CTCCCGGGCAGCTGCGCCGAGCAA	2678	
Qy	3141	CGG	CTCTG	CAAGCGTCTCAGAG	CCCTGTGCGGCTCC	ACCATCTCTCGCCCGCTCGTC	3200	
Ds	2679	CGT	CTCCG	CAAGCGGTTCAG	CAGCCCTTGGAGGCTCC	AGGATCCACCCCTTCTCTCTC	2738	
Qy	3201	CAC	CTCGG	CCCGGCTCAC	CATGAGATG	CAGCGCTG	CAGCAGCAAGGTCA	3260
Ds	2739	CAT	CAGCA	CAAGCAACA-----	CGAAGAC	CCATTTCCCA	CAGCCGAGGAGCAAG	2793



2061	Qy	CTCAAAGTGGTTCCTTTCTCCAACTGCAGTCGAGACTGTGTCCGGGACCAAGGAAGG	2120	Qy	GTCTGCTCTTCCCTCATCTGCTCTTCCAGTCTGGCATCTGCATGTCGAGAGGAGATT
1627	Db	CTCCAGGGAGGTGCCCTTCTTCCAACTGCAGCCGAGACTGCCTGGCAGGACCAAGGAAAG	1686	Db	GATCATCGAGGGGAGCCCACTTCCTGCTTTGAATGATCGCATGTGCAGAGGAGATT
2121	Qy	GATCATCGAGGGGAGCCCACTTCCTGCTTTGAATGATCGCATGTGCAGAGGAGATT	2180	Qy	GATCATCGAGGGGAGCCCACTTCCTGCTTTGAATGATCGCATGTGCAGAGGAGATT
1687	Db	GATCATCGAGGGGAGCCCACTTCCTGCTTTGAATGATCGCATGTGCAGAGGAGATT	1746	Db	CAGTGATGAAAAAGATGCAAGTGCCTGTACAAAGTGCCTCGAATGTCTGTGTCGAATGA
2181	Qy	CAGTGATGAAAAAGATGCAAGTGCCTGTACAAAGTGCCTCGAATGTCTGTGTCGAATGA	2240	Qy	TAGTGATGAGACAGATGCCAGTGCCTGTAAACAAGTGCCTCAGATGACTTCTGTGTCGAATGA
1747	Db	TAGTGATGAGACAGATGCCAGTGCCTGTAAACAAGTGCCTCAGATGACTTCTGTGTCGAATGA	1806	Db	GAACCAACACTCTCGATTTGCCAAGAGATCGAGTTTCTGTCTGTGAGAGGAGCCCTTGG
2241	Qy	GAACCAACACTCTCGATTTGCCAAGAGATCGAGTTTCTGTCTGTGAGAGGAGCCCTTGG	2300	Qy	GATCGACTCACCTCTTTGCCGTGTGGCATTTTCTTGACAGCCCTTGTGTGGGTGT
1807	Db	GAACCAACACTCTCGATTTGCCAAGAGATCGAGTTTCTGTCTGTGAGAGGAGCCCTTGG	1866	Db	GATCGACTCACCTCTTTGCCGTGTGGCATTTTCTTGACAGCCCTTGTGTGGGTGT
2301	Qy	GATCGCTTGACCATCTTCGCCCTACTGGGCATCTTGATCACCTCTTGTGTGGGGT	2360	Qy	CCTTTCATCAAGTTTCAAGAACACTCCCATCTGTTGAAGGCCACCAACGGGAGTTGTCTACCT
1867	Db	GATCGACTCACCTCTTTGCCGTGTGGCATTTTCTTGACAGCCCTTGTGTGGGTGT	1926	Db	GATCGACTCACCTCTTTGCCGTGTGGCATTTTCTTGACAGCCCTTGTGTGGGTGT
2361	Qy	CCTTTCATCAAGTTTCAAGAACACTCCCATCTGTTGAAGGCCACCAACGGGAGTTGTCTACCT	2420	Qy	GATCGACTCACCTCTTTGCCGTGTGGCATTTTCTTGACAGCCCTTGTGTGGGTGT
1927	Db	GATTCATCAAGTTTCCGCAACACAACCATGTTCAAGGCCACCAACGGAGAGTCTTCTACCT	1986	Db	GATTCATCAAGTTTCCGCAACACAACCATGTTCAAGGCCACCAACGGAGAGTCTTCTACCT
2421	Qy	GCTGCTCTTCTCCCTCATCTGCTCTTCCAGTCTGGCTCATCTTCATCGCGAGCCCAAG	2480	Qy	GCTGCTCTTCTCCCTCATCTGCTCTTCCAGTCTGGCTCATCTTCATCGCGAGCCCAAG
1987	Db	CCTCTCTTCTCCCTGTCTGCTGCTCTCCAGTCTCCCTGTTCTTATCGGGAGCCCA	2046	Db	CCTCTCTTCTCCCTGTCTGCTGCTCTCCAGTCTCCCTGTTCTTATCGGGAGCCCA
2481	Qy	GGACTGGAACCTGTGGCTTCGCCAAACGGGCTTTGGCATCAGCTTCGTCTGTGCATCTC	2540	Qy	GGACTGGAACCTGTGGCTTCGCCAAACGGGCTTTGGCATCAGCTTCGTCTGTGCATCTC
2047	Db	GGACTGGAACCTGTGGCTTCGCCAAACGGGCTTTGGCATCAGCTTCGTCTGTGCATCTC	2106	Db	GGACTGGAACCTGTGGCTTCGCCAAACGGGCTTTGGCATCAGCTTCGTCTGTGCATCTC
2541	Qy	CTGCATCTCTGGTGAAGAACCAACGGGTCTGCTGCTTCTGAGGCCAAGATCCCCACCAG	2600	Qy	CTGCATCTCTGGTGAAGAACCAACGGGTCTGCTGCTTCTGAGGCCAAGATCCCCACCAG
2107	Db	ATGCATCTCTGGTGAAGAACCAACGGGTCTTCTGTTGTTTGAAGGCCAAGATCCCCACCAG	2166	Db	ATGCATCTCTGGTGAAGAACCAACGGGTCTTCTGTTGTTTGAAGGCCAAGATCCCCACCAG
2601	Qy	CCTCCACCGCAAGTGGGTGGGCTCAACCTGCAGTTCCTCCTGGTCTTCCTTGCATCTCT	2660	Qy	CCTCCACCGCAAGTGGGTGGGCTCAACCTGCAGTTCCTCCTGGTCTTCCTTGCATCTCT
2167	Db	CTTCCACCGCAAGTGGGTGGGCTCAACCTGCAGTTCCTCCTGGTCTTCCTTGCACCTT	2226	Db	CTTCCACCGCAAGTGGGTGGGCTCAACCTGCAGTTCCTCCTGGTCTTCCTTGCACCTT
2661	Qy	GGTGCAATCGTACCTGCATCTAGCTCTACACCGCCCTCCCTCAGCTTACAGGAA	2720	Qy	GGTGCAATCGTACCTGCATCTAGCTCTACACCGCCCTCCCTCAGCTTACAGGAA
2227	Db	CATGCAGATTGTATCTGTGTGATCTGGCTCTACACCGCCCTCCCTCAGCTTACAGGAA	2286	Db	CATGCAGATTGTATCTGTGTGATCTGGCTCTACACCGCCCTCCCTCAGCTTACAGGAA
2721	Qy	CCATGAGCTGGAGGACGAGGTCTATCTTCATCACCTGCGAGAGGGTTCGTCTATGGCGT	2780	Qy	CCATGAGCTGGAGGACGAGGTCTATCTTCATCACCTGCGAGAGGGTTCGTCTATGGCGT
2287	Db	CCAGGAGCTGAGGATGAGATCATCTTTCATCACCTGCGACAGGGGTCCCTCATGGCCCT	2346	Db	CCAGGAGCTGAGGATGAGATCATCTTTCATCACCTGCGACAGGGGTCCCTCATGGCCCT
2781	Qy	GGGGTTCCTCATCGGCTACACCTTGCTCTCGCGCCATCTGCTTCTTTCGCCCTCAA	2840	Qy	GGGGTTCCTCATCGGCTACACCTTGCTCTCGCGCCATCTGCTTCTTTCGCCCTCAA
2347	Db	GGGGTTCCTCATCGGCTACACCTTGCTCTCGCGCCATCTGCTTCTTTCGCCCTCAA	2406	Db	GGGGTTCCTCATCGGCTACACCTTGCTCTCGCGCCATCTGCTTCTTTCGCCCTCAA
2841	Qy	GTCCGCTAAGCTGCCGAGAACTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTTGAT	2900	Qy	GTCCGCTAAGCTGCCGAGAACTCAACGAGGCTAAGTTTCATCACCTTCAGCATGTTGAT
2407	Db	GTCCCGAAGCTGCCGAGAACTCAATGAAGCCAGTTTCATCACCTTCAGCATGCTCAT	2466	Db	GTCCCGAAGCTGCCGAGAACTCAATGAAGCCAGTTTCATCACCTTCAGCATGCTCAT
2901	Qy	CTTCTTCATCGTCTGATATCTCCTTCATCCCGGCTATGTGAGCACCTACCGGAAGTTTGT	2960	Qy	CTTCTTCATCGTCTGATATCTCCTTCATCCCGGCTATGTGAGCACCTACCGGAAGTTTGT
2467	Db	CTTCTTCATCGTCTGATATCTCCTTCATCCCGGCTATGTGAGCACCTACCGGAAGTTTGT	2526	Db	CTTCTTCATCGTCTGATATCTCCTTCATCCCGGCTATGTGAGCACCTACCGGAAGTTTGT
2961	Qy	GTGGGCGGTGGAGTGATTCGATCTCGGCTCCAGCTTCGGGTGCTGGGCTGCAATTA	3020	Qy	GTGGGCGGTGGAGTGATTCGATCTCGGCTCCAGCTTCGGGTGCTGGGCTGCAATTA
2527	Db	CTCTGCGGTGAGGTGATTTGCCATCTCTGGCAGCCAGCTTTGGCTTGTGCGGTGCACTT	2586	Db	CTCTGCGGTGAGGTGATTTGCCATCTCTGGCAGCCAGCTTTGGCTTGTGCGGTGCACTT
3021	Qy	CTTCAAACAAGTTTACATCATCTCTGTTTCAAGCGGTGCCGTAACAACATCGAGAGGTGG	3080	Qy	CTTCAAACAAGTTTACATCATCTCTGTTTCAAGCGGTGCCGTAACAACATCGAGAGGTGG
2587	Db	CTTCAAACAAGCTATACATCATCTCTTCAAGGCCATCCCGCAACACCATCGAGAGGTGG	2646	Db	CTTCAAACAAGCTATACATCATCTCTTCAAGGCCATCCCGCAACACCATCGAGAGGTGG
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RESULT 15
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; GENERAL INFORMATION: CATHERINE E.
; APPLICANT: ELLIS,
; TITLE OF INVENTION: MONKEY CALCIUM SENSING RECEPTOR
; FILE REFERENCES: GP-70685
; CURRENT APPLICATION NUMBER: US/09/727,205
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,342
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: MACACA CYNOMOLGUS
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				Gaps 3;

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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8: gb\_gss1:  
9: gb\_gss2:  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	495.4	12.0	637	9 CE303215	tigr-gss-
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6	440.2	10.6	579	6 CD608332	56076771J
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9	415.2	10.0	654	6 CD608330	56048444J
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13	336.4	8.1	567	5 BP766221	BP766221
14	329.8	8.0	776	7 CK483822	AGENCOURT
15	313.8	7.6	653	2 BB615858	BB615858
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20	246.2	6.0	923	4 BJ730259	BJ730259
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22	233.6	5.7	525	9 CC546019	CH240_428
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ALIGNMENTS

RESULT 1  
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LOCUS 3115 bp mRNA linear HTC 03-APR-2004  
DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:493054218 product:calcium-sensing receptor, full insert sequence.  
ACCESSION AK029770  
VERSION AK029770.1 GI:26325707  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
93273253  
10349636  
REFERENCE 2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159  
REFERENCE 3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

REFERENCE 4  
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 688-690 (2001)  
REFERENCE 5  
The FANTOM Consortium and the RIKEN Genome Exploration Research

TITLE	Group Phase I & II Team	QY	1339	GAGGCTTGGGCCAGCTCTTTCGCTCATTTGCCAAGCCAGAGTACTTCCACGCTGGTGGCGGC 1398
JOURNAL	Analysis of the mouse transcriptome based on functional annotation	Db	1	1 GAGGCTTGGGCCAGTTCCTCCCTGATTTGCTATGCTGAGTACTTCCATGAGTGGGGT 60
REFERENCE	Nature 420, 563-573 (2002)	QY	1399	ACCATGGCTTCCGCTCTCAGGGGGGGGCTATCCCAAGGGTTCAACAAGTTCCTGGAAGGAG 1458
AUTHORS	Adachi, J., Aizawa, K., Anikura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Iotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	Db	61	ACCATTGGGTTGCTGCTGAAGGCTGGGCGAGTTCCAGGCTTCGAGAAATTCCTACAGAAA 120
	Direct Submission	QY	1459	GTCACCCAGCAGAGTCTCCGACAAATGGTTTGTCAAGAGTTCTGGGAGAGAGACTTC 1518
	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	Db	121	GTCCATCCAGGAGTCTGTCTCAATGGTTTTCCTCAAGAGTTTGGGAGAGAAATTT 180
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	QY	1519	AACCTGCTACTTCCACGAGAGACCTCTGACGAGCTGAAGAATTCAGAGTGGCCCTCGCAC 1578
	Please visit our web site for further details.	Db	181	AATTGC-----CACCTGCAAGACGGCGCAAAAGGAGCTTTACCGCTGGACACCTTCGTGA 235
	URL: http://genome.gsc.riken.jp/	QY	1579	GGACCGGCGCTCAAGGGGAGCGCTCCAGGGGGGAACTCCAGACGGACAGCCCTACGC 1638
	URL: http://fantom.gsc.riken.jp/	Db	236	GAA-----GTCCAGGAGGAGCGGCAAGGTTACTCAATAGCTTCCACTGCTTCCGA 288
FEATURES	Location/Qualifiers	QY	1639	CACCCCTGCACTGGGAGGAGAAATCACCAGCGTGGAGACCCCTTACCTGGATTATACA 1698
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	/dev_stage="adult"	Db	589	AACCTGCGAGCTCTCCGACAGGAGCTCCATTTGTTTCAAGGAAGTTGGGTACTACAAT 648
CDS	<1..2352	QY	1999	GCCTAGCTAAGCCAGTACGAGTCAACATCAACGAAAGAAATCTCTGGAGTGGC 2058
	/note="unnamed protein product; calcium-sensing receptor (MGD) [MG1:1351351, GB NM_013803, evidence: BLASTN, 99%, match=3113]	Db	649	GTGTATGCCAAGAGGAGAGAGACTGTTCATCAATGAGGGGAAGATCTTTGGAGTGGG 708
	putative"	QY	2059	TTCTCCAAAGTGGTCTCTTCTCCAACTGCGAGTCAAGATGTGTGCGGGGACCCAGGAAG 2118
	/codon_start=1	Db	709	TTCTCCAGAGGTTGCCCTTCTCCAACTGACGCGGAGCTGTTCAGGACGGGACCGAAG 768
	/protein_id="BAC26608.1"	QY	2119	GGGATCATCGAGGGGAGCCCTCTGCTTGTGAATGATGCGCATGTGAGAGGAGAG 2178
	/db_xref="GI:26325708"	Db	769	GGCATCATTCAGGAGAGCCCTCTGCTGTTTGAAGTGTGAGTGTGAGTGTCTGAGCGCGAG 828
	/translation="EAWASSSLIAMPFHHVVGTTIGFLKAGQIPGPREFLQKVRP KSVHNGFAKEWEEFNCHLDGAKGKPLVDTFVRSHEEGNRLNLSSTAFRLCTGD ENINSVETPYMDIEHLISYNYLVAVSIAHALQDIYCLPGRGLFTNGSCADIKVY AMOVLKHLHLNLTNNQGEQVTFDECGDLVGNYSILNNHLSPEGDSIVPEKVGNYVY AKKGRFLFNEGKILWSGFEVPSNCSRCQAGTRKGIIEGPTCCFEVCEPDGE YSGEDTASACKPDFFSNENHTSIKAEIEFLAWEPTFGIATLFAVIGLITAFV LGVFTKFNTPITVRLNLELYLLSLLCCFSFFLIEGPQDMTRLRQPAFGISF VLICISLIVKTNVLEFAKIPTSFRKMGWLNQFLVFLCTFMQIVICIIWLYTA PPSVYRNELEDEIPIFTCHESLMALGLIGYTCILAAICFFPAFKSRKLPENFNA KXITFTSMILFFVTWISFTPAVASTYKFVSAVEITAAASFGLLACIFFNKVYIILF XPSRNTISEVRSCTAAHAKVAARATLRPNISRSKSSLSGSGTSIPSSSISKSN EDKFPQPRKQKQPLATQEQOQPLTLQEQOQOQPRCKQKQIFGSGVTFSI SDFEPQKNAMHRNSQNSLEAQNSDNLNRHQLLPQCAEADSEMTIOETLQGP MVGDQPIESPDENSPALVMTSVSRFSVISGGSGSVTENILHS"	QY	2179	TTCAAGTGTGATGAAAACGATGCAAGTGGGTGTACAAAGTGCCTCCCAATGATTTCTGGTCCAAT 2238
		Db	829	TACAGTGGTGAGACAGATGGAGTGTCTGTGACAAAGTGCCTGAGTGTGAGTGTCTGAGCGCGAG 888
		QY	2239	GAGAACACACGCTGTCATCGCAAGGAGATCGAGTACTGTGTFGAGAGGAGCCCTTC 2298
		Db	889	GAGAACACACTTCTCTGCAATGGCAAGGAGATGAGTCTCTGCGCTGGAGTGTGAGCGCTTT 948
		QY	2299	GGGATCGCTGAGCACTTTCGCGTACTGGGATCCTGATCACCTCTTCTGCTGGGGG 2358
		Db	949	GGAAATCGCTCTACTCTCTTGGGGTGTGGGCAATTTTCTGACCGCCCTTGTGCTGGGG 1008
		QY	2359	GTCTTTCATCAAGTTTCAGGAACACTTCCCATCGTGAAGGCCAACCAACCGGAGTTGTCTTAC 2418
		Db	1009	GTCTTTCATCAAGTTTCAGGAACACTTTCAGGCGCCCAATGTCAAGGCCAACCAACCGAGAGTGTCTTAC 1068
		QY	2419	CTGCTGCTCTTCTCCCTCATCTGCTGCTCTCCAGCTCGTCTCATCTTCATCGCGAGGCC 2478

ORIGIN

Query Match 28.3%; Score 1171.4; DB 3; Length 3115;

Best Local Similarity 77.1%; Pred. No. 3e-251;

Matches 1456; Conservative 0; Mismatches 421; Indels 12; Gaps 2;



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QY      2901 CTTTC 2904
Db      742 CTTTC 745

RESULT 3
LOCUS   CE057025          746 bp DNA linear GSS 24-SEP-2003
DEFINITION tigr-gss-dog-17000322442684 Dog Library Canis familiaris genomic,
ACCESSION CE057025
VERSION   CE057025.1 GI:35104961
KEYWORDS  GSS.
SOURCE    Canis familiaris (dog)
ORGANISM  Canis familiaris
REFERENCE 1 (bases 1 to 746)
AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
          Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
          Venter,J.C.
          The dog genome: survey sequencing and comparative analysis
TITLE     The dog genome: survey sequencing and comparative analysis
JOURNAL   Science 301 (5641), 1898-1903 (2003)
MEDLINE   22875432
PUBMED    14512627
COMMENT   Contact: Kirkness EF
          The Institute for Genomic Research
          Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
          Rockville, MD 20850, USA
          Tel: 301-838-0208
          Fax: 301-838-0208
          Email: ekirknes@tigr.org
          Class: shotgun.

FEATURES             Location/Qualifiers
     source           1..746
     organism="Canis familiaris"
     /mol_type="genomic DNA"
     /strain="Standard Poodle"
     /db_xref="taxon:9615"
     /clone_lib="Dog Library"
     /note="Site 1: BstXI; Libraries were prepared from
     peripheral blood"

ORIGIN
Query Match 13.0%; Score 535.4; DB 9; Length 746;
Best Local Similarity 84.6%; Pred. No. 8.5e-109;
Matches 613; Conservative 0; Mismatches 111; Indels 1; Gaps 1;

QY      2181 CAGTCATGAACGATGCGTGTACAAAGTGGCCGGAATGATTTCTGGTGGATGA 2240
Db      742 CTTTC 745

QY      2241 GAAACACACGTCGTGCATCGCCAGAGATCGAGTACCTGTCTGGAGCGGCCCTTCGG 2300
Db      82 AAACACACACTTCGTGCAATGCCAAGAGATTGAGTTCTGTCTGGACAGACCCCTTGG 141

QY      2301 GATCCTCTGACCATCTTCGGCTACTGGGATCTGATACCTCTTCGTCTGGTGGGGT 2360
Db      142 GATTCACATCAACCTCTTTTGTGTGTCTGGGATTTTCCTGACAGCTTCGTCTGGGGGT 201

QY      2361 CTTTCATCAAGTTTCAGGAACACTCCCATCGTGAAGCCACCAACCGGAGTTGCTCTACCT 2420
Db      202 CTTTCATCAAGTTTCAGGAACACTCCCATCGTGAAGCCACCAACCGGAGTTGCTCTACCT 261

QY      2421 GCTGCTCTTCCTTCATCTGCTGCTTCCTCAGCTTCGCTCATCTTCATCGCGGAGCCCGAG 2480
Db      262 CTTCTCTCTCTCTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 321

QY      2481 GGACTGGACCTGTGGCTCCGCCACCGGCTTTGGGATCAGCTTCGCTCTGTCATCTC 2540
Db      322 GGACTGGACCTGTGGCTCCGCCACCGGCTTTGGGATCAGCTTCGCTCTGTCATCTC 381

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QY      2541 CTGCATCTCTGGTGAAGACCAACCGGGTGTCTGTGTTCTTCGAGGCCAAGATCCCCACAG 2600
Db      382 ATGCATCTCTGGTGAAGACCAACCGGTGTCTGTCTGTGTTCTTCGAGGCCAAGATCCCCACAG 441

QY      2601 CTTCCACCGCAAGTGGGTGGGCTCAACCTGCAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2660
Db      442 CTTCCACCGCAAGTGGTGGGGCTCAACCTGCAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 501

QY      2661 GGTGCAAAATCGTCACTGCATCATCTGGCTCTACACCGGCGCTCTCTCTCTCTCTCTCTCTCT 2720
Db      502 CATGCGAATGTCTATCTGTGTGATCTGGCTCTACACGGGCGCTCTCTCTCTCTCTCTCTCTCT 561

QY      2721 CCATGAGCTGGAGGACGAGGTCTATCTTCATCACTCGACGAGGGCTCGCTCATGGCGCT 2780
Db      562 CCATGAGCTGGAGGACGAGATCATCTTCATCATGCCACGAGGGCTCTCTCTCTCTCTCTCTCT 621

QY      2781 GGGCTTCTCATCGGCTACACCTGCTCTCTCGCGGCATCTGCTCTCTCTCTCTCTCTCTCTCTCT 2840
Db      622 GGGCTTCTCATCGGCTACACCTGCTCTCTCGCGGCATCTGCTCTCTCTCTCTCTCTCTCTCTCT 681

QY      2841 GT-CCGTAAGTCCGAGAACTTCAACGAGGCTAAAGTTTCATCAGCTTCAGCATGTTCA 2899
Db      682 GTCCCGGAGCTGCCGAGAACTTCAACGAGGCTAAAGTTTCATCAGCTTCAGCATGTTCA 741

QY      2900 TCTTC 2904
Db      742 TCTTC 746

RESULT 4
LOCUS   CE303215          637 bp DNA linear GSS 26-SEP-2003
DEFINITION tigr-gss-dog-17000360222011 Dog Library Canis familiaris genomic,
ACCESSION CE303215
VERSION   CE303215.1 GI:36094287
KEYWORDS  GSS.
SOURCE    Canis familiaris (dog)
ORGANISM  Canis familiaris
REFERENCE 1 (bases 1 to 637)
AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
          Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
          Venter,J.C.
          The dog genome: survey sequencing and comparative analysis
TITLE     The dog genome: survey sequencing and comparative analysis
JOURNAL   Science 301 (5641), 1898-1903 (2003)
MEDLINE   22875432
PUBMED    14512627
COMMENT   Contact: Kirkness EF
          The Institute for Genomic Research
          Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
          Rockville, MD 20850, USA
          Tel: 301-838-0208
          Fax: 301-838-0208
          Email: ekirknes@tigr.org
          Class: shotgun.

FEATURES             Location/Qualifiers
     source           1..637
     organism="Canis familiaris"
     /mol_type="genomic DNA"
     /strain="Standard Poodle"
     /db_xref="taxon:9615"
     /clone_lib="Dog Library"
     /note="Site 1: BstXI; Libraries were prepared from
     peripheral blood"

ORIGIN
Query Match 12.0%; Score 495.4; DB 9; Length 637;
Best Local Similarity 87.1%; Pred. No. 7.6e-100;
Matches 555; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

QY      2408 AGTGTCTTACTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2467

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/note="Vector: pDrive Cloning Vector"

ORIGIN

Query Match 10.6%; Score 440.2; DB 6; Length 579;  
Best Local Similarity 87.0%; Pred. No. 1.8e-87;  
Matches 495; Conservative 0; Mismatches 73; Indels 1; Gaps 1;

QY 2407 GAGTTCCTACTGCTGCTCTCTCTCCCTCACTCTGCTGCTCTCCAGCTCGCTCATCTTC 2466  
Db |||||  
QY 578 GAGCTCTCTACT 519  
Db |||||  
QY 2467 ATCGGAGCCAGGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2526  
Db |||||  
QY 518 ATCGGAGCCAGGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 459  
QY 2527 GTCTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2586  
Db |||||  
QY 458 GTGCTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 399  
Db |||||  
QY 2587 AGATCCCCACAGCTCTCCACCGCAAGTGGGTGGGCTCAACTGCGATTCCTCTGCTGCT 2646  
Db |||||  
QY 398 AGATCCCCACAGCTCTCCACCGCAAGTGGGTGGGCTCAACTGCGATTCCTCTGCTGCT 339  
QY 2647 TTCCTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2706  
Db |||||  
QY 338 TTCCTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 279  
QY 2707 TCAGCTCAGGAACCATGAGCTGGAGGAGGAGTCACTTCACTGAGCTGAGCTGAGCTGAG 2766  
Db |||||  
QY 278 TCAGCTCAGGAACCATGAGCTGGAGGAGGAGTCACTTCACTGAGCTGAGCTGAGCTGAG 219  
QY 2767 TCCTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2826  
Db |||||  
QY 218 TCCTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 160  
QY 2827 TTCCTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2886  
Db |||||  
QY 159 TTCCTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 100  
QY 2887 TTCAGATCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2946  
Db |||||  
QY 99 TTCAGATCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 40  
QY 2947 TAGGGAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2975  
Db |||||  
QY 39 TAGGGAAGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 11

RESULT 7

CE504040/c  
LOCUS tigr-gss-dog-17000327352242 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CE504040  
VERSION CE504040.1 GI:36820821  
KEYWORDS GSS  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 670)  
AUTHORS Kirchner, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,  
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and  
Venter, J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
MEDLINE 22875432  
PUBMED 14512627

COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200

FEATURES

source  
1. 670  
Location/Qualifiers  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/notes="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

ORIGIN

Query Match 10.4%; Score 431.6; DB 9; Length 670;  
Best Local Similarity 84.5%; Pred. No. 1.6e-85;  
Matches 485; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 2194 GATGCAAGTCGCTGATCAAAAGTCCCGAATGATTTCTGCTGCAATGAGAACCAACACGTCG 2253  
Db |||||  
QY 574 GATGCAAGTCGCTGATCAAAAGTCCCGAATGATTTCTGCTGCAATGAGAACCAACACGTCG 515  
QY 2254 TGATGCCCAAGAGATCGAGTACCTGCTGCGACCGAGCCCTTCGGATCGCTCGACC 2313  
Db |||||  
QY 514 TGCATTGCCCAAGAGATGAGTTTCTGCTGCGACAGAGCCCTTTGGGATTGCACTCACC 455  
QY 2314 ATCTTCGCCGTACTGGGCATCTCTGATCAGCTCTCTGCTGGGGTCTTTCATCAAGTTTC 2373  
Db |||||  
QY 454 CTCTTTGCTGTCTGGGCATTTCTGACAGCTTTCGCTGGGGTCTTTCATCAAGTTTC 395  
QY 2374 AGGAACACTCCCATGTAAGGCCACCAACCGGAGTTTCTGCTGCTGCTGCTGCTGCTGCT 2433  
Db |||||  
QY 394 CGTAACACGCCATCGTCAAGGCCACCAACCGGAGTTTCTGCTGCTGCTGCTGCTGCTGCT 335  
QY 2434 CTATCTGCTGCTTCTCCAGCTGCTCATCTTCATCGGAGCCAGGAGCTTGACCTGT 2493  
Db |||||  
QY 334 TTGCTGTGCTTCTCCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 275  
QY 2494 CGGCTCGGCAACCGGCTTTGGCATCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2553  
Db |||||  
QY 274 CGCTCGGCGAGCGGCTTTGGCATCAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 215  
QY 2554 AAGACCAACCGGCTGCTGCTTTCGAGGCCAAGATCCCGACCGCTCCACCGCAG 2613  
Db |||||  
QY 214 AAAACCAACCGTGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 155  
QY 2614 TGGGTGGGGCTCAACCTGAGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2673  
Db |||||  
QY 154 TGGTGGGGCTCAACCTGAGTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 95  
QY 2674 ACTGTGATCTGCTGCTTACACCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2733  
Db |||||  
QY 94 ATCTGTGTGATCTGCTGCTTACACCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 35  
QY 2734 GAGCAGTCTATCTTCACTACCTGCGAGGGGT 2767  
Db |||||  
QY 34 GAGCAGTCTATCTTCACTACCTGCGAGGGGT 1

RESULT 8

CD608327/c  
LOCUS CD608327 600 bp mRNA linear EST 12-JAN-2004  
DEFINITION S6021515H1 FLP Homo sapiens cDNA, mRNA sequence.  
ACCESSION CD608327  
VERSION CD608327.1 GI:40256590  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 600)  
AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Yang, J. and Stuve, L.L.  
TITLE Circular rapid amplification of cDNA ends for high-throughput

Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.







```

RESULT 12
CK805060
LOCUS
DEFINITION
AGENCOURT 19147865 NICHX XGC Te2 Xenopus laevis cDNA clone
IMAGE:7211077 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus;
1 (bases 1 to 813)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Igor B. Dawid
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLaM15101 row: c column: 11
High quality sequence start: 9
High quality sequence stop: 695.
Location/Qualifiers
1..813
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:7211077"
/tissue_type="Pooled samples from 6 adult Xenopus testis"
/lab_host="DH10B TonA"
/clone_lib="NICHX XGC Te2"
/note="Organ: testis; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; RNA obtained from 6 adult male testis. cDNA
was primed using oligo-dT primer:
5'-pGACTAGTCTAGTCGGAGCGCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1kb
resulted in an average insert size of 1.25 kb. This is a
primary library (normalized primary library is
NICHX XGC Te2N) and was constructed by Express Genomics
(Fredrick, MD). Note: this is a NIH_MGC library"
ORIGIN
Query Match 8.9%; Score 369; DB 7; Length 813;
Best Local Similarity 73.0%; Pred. No. 1.8e-71;
Matches 474; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 1733 TCTACTCCATTGCTACGCCCTGCAAGACATCCACTCTTTGCAAAACCCGCGACGGCATCT 1792
DB 13 TCTCCGGATCGCTTATGCTTGTGACAGATATATCTCTGACCCCTGGGAAGGGCTGT 72
QY 1793 TTGCAACAGGATCTTGTGAGATATTAAAAAAGTTGAGCCCTGGGAGGTCCTCAACCATC 1852
DB 73 TTGCCAACAAATTCCTGTGCCGACATAAAGAAAGTGAAGCCTGGCAGTTGCTGAAACACT 132
QY 1853 TCGTGCATCTGAGTTTACACAGCATGGTGACGAGTTTACATTTGACGATCAGGTG 1912
DB 133 TGGCGCATCTCAATTTTCAACACATATGGGGAGCAGGTGGACTTCATGACTCAGGGG 192
QY 1913 ACCTCAAGGGGAACACTACACATTATCACTGGCAGCTCTCCGACAGGATGATCGGTGT 1972
DB 193 ACCTGTGGGAACACTACTCCATCATCACTGCGACCTGTGCAAGGAGGACACTCCATTG 252

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QY 1973 TGTTCATGAGGTGGGCAACTACAGCCTACGCTAAGCCAGTACCGACTCAACATCA 2032
DB 253 TGTTCGAGGAGGTGGGGTACTACACGCTCTATGCCAAGGTGGCGGAGCGGCTTTTCATCA 312
QY 2033 ACCAAAGAAAATCCCTCTGGAGTGGCTTCTCCAAAGTGGTTCCTTTCTCCAACTGCAGTC 2092
DB 313 ACGAAGCAAAATCCCTGTGGAGAGGCTTCTCCGAGTGGTCCCAATTTCCAACTGCAGTC 372
QY 2093 GAGACTGTGTGCGGGGACCAGGAAGGGGATCATCGAGGGGGAGCCACCTGTCTGTGTTG 2152
DB 373 AAATCTGCCAGGAAGGCAACCCGGAAGGATCATTTGAAGGGAACCACTGTCTGTGTTG 432
QY 2153 AATGCATGGCATGTGCAGAGGGAGAGTTCAGTGCATGATGAAACGATGCAAGTGCCTGTACAA 2212
DB 433 AATGTGTTGACTGCCCGACGGGATACAGTGTATGACAGATGCCAGTGCCTGTGAGA 492
QY 2213 AGTCCCGAATGATTTCTGTGTCGAATGAGAACACACACGTCGTGCATCGCCAGGAGATCG 2272
DB 493 AATGTGCCAAGGATTAATGTTGTCATGMAAACACACACTTCTGCAITTCGACAGATCG 552
QY 2333 TCTGATCACCTCTTCTGCTGGGGTCTTCAATCAAGTTTCAGGAACAC 2381
DB 613 TATGTCATCTTCAATTTGTTCTCGGTGTTTTCATCAAAATTCGCAACAC 661

RESULT 13
BP766221
LOCUS
DEFINITION
BP766221 mouse (C57BL/6) pancreatic islet library with
recombination-based method Mus musculus cDNA clone mid09082 5',
mRNA sequence.
ACCESSION
VERSION BP766221.1 GI:50224919
KEYWORDS
SOURCE
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 567)
Nishimura, M., Yokoi, N., Miki, T., Horikawa, Y., Yoshioka, H.,
Takeda, J., Ohara, O. and Seino, S.
TITLE
Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL
Unpublished (2004)
COMMENT
Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1..567
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="mid09082"
/sex="male"
/tissue_type="pancreatic islet"
/dev_stage="adult"
/clone_lib="mouse (C57BL/6) pancreatic islet library with
recombination-based method"
ORIGIN
Query Match 8.1%; Score 336.4; DB 5; Length 567;
Best Local Similarity 76.6%; Pred. No. 3.3e-64;
Matches 412; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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1727 TGCCCGTCTACTCCATTGCTCAGCCCTGCAAGACATCCACTCTTGCAAAACCGGCAAGG 1786
Db 30 TAGCCGCTCTACTCCATTGCGCAGCCCTGCAAGATATATACACTCTGTTACCGGAAGAG 89

1787 GCATCTTTGCAACGAGATCTTGCGAGATATTAATAAGTTGAGGCTTGCGAGGTCCTCA 1846
Db 90 GGCTTTTTCACCAACGAGGCTCTGTCAGACATCAAGAAGTTTGAGGCTTGCGAGGTCCTGA 149

1847 ACCATCTGTGATCTGAAATTTACCAACAGATGGTGGAGGTTGACTTTGACGATC 1906
Db 150 AACACCTAGGCACCTGAAATTTACCAACATGGGGAGGAGGTGACCTTCGATGAGT 209

1907 AAGTGACCTCAAGGGGAATCAACATTTATCAACTGGCAGTCTCCGAGAGGATGAAT 1966
Db 210 GGGGTGACCTGGTGGGAATCACTCCATCATCAACTGGCACCTCTCCGAGAGGACGGCT 269

1967 CGGTGTTGTTCCATGAGTGGCAACTACACGCTTACGCTAAGCCGAGTGACGACTCA 2026
Db 270 CAATTGTTTCAAGGAAGTTGGGTACTCAATGTGTATGCCAAGAGGAGAAAGACTGT 329

2027 ACATCAACGAAAGAAATCTCTGAGTGGCTTCTCCAAAGTGTCTCTTCTCCAACT 2086
Db 330 TCATCAATGAGGGGAAGATCTTGTGGAGTGGTCTCCAGAGAGGTGCGCTTCTCCAACT 389

2087 CGAGTCGAGACTGTGTCGGGCAACAGGAAGGGAGTCAATCGAGGGAGGCCCACTGCT 2146
Db 390 GCAGCCGGGACTGTTCAGGCGAGGACAGGAAGGGCATCATTTAGGAGAGGCGCCACTGCT 449

2147 GCTTTCAATGCGATGCGATGTGCGAGAGGAGAGTTCAGTGAATGAAACGATGCAAGTGGT 2206
Db 450 GTTTTGAAGTGTGGAGTGTCTGAGCGGAGTACAGTGGTGAGACAGATGCGAGTGGCT 509

2207 GTACAAAGTGGCGGAATGATTTCTGTCGAATGAGAACACACGTCGTGTCATCGCCAA 2264
Db 510 GTGACAAAGTGGCGGATGATCTTGTGTCGAATGAGAACACACACTTCTGTCATGCGCAA 567

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RESULT 14
LOCUS CK483622
DEFINITION AGENCOURT_17636458 NIH_MGC_235 Rattus norvegicus cDNA clone
IMAGE:7109300 5', mRNA sequence.
CK483622
CK483622.1 GI:40827970
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 776)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999).
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gcapbs@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
DNA Sequencing by: The I.M.A.G.E. Consortium (ILLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
Plate: LL4W14974 row: j column: 18
High quality sequence stop: 590.
Location/Qualifiers
1. .776
/organism="Rattus norvegicus"
/mol_type="mRNA"

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```

FEATURES
source

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/db xref="taxon:10116"
/clone="IMAGE:7109300"
/tissue_type="kidney, pooled"
/lab_host="DH10B Tona"
/clone_lib="NIH_MGC_235"
/notes="Organ: kidney; Vector: pExpress-1; Site: 1. EcorV;
Site: 2. NotI; RNA obtained from pooled kidney tissue from
a mix of male and female animals at 8 wk old. Tissues were
snap-frozen before RNA extraction and purification
(Tri-reagent method). cDNA was primed using oligo-dT
primer: 5'-pGACTAGTCTAGATCGGAGCGGCCCT(T)25-3' and
cloned into the EcorV/NotI sites of pExpress-1.
Size-selection >1.4kb resulted in an average insert size
of 2.2 kb. This primary library is non-normalized
(normalized primary library is NIH_MGC_236) and was
constructed by Express Genomics (Frederick, MD). Note:
this is a NIH_MGC library."

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ORIGIN

```

Query Match      8.0%; Score 329.8; DB 7; Length 776;
Best Local Similarity 69.0%; Pred. No. 1.1e-62;
Matches 524; Conservative 0; Mismatches 232; Indels 15; Gaps 4;

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QY 1072 TGGGTGGAAACCTTGGCAGCCGATGACTATATGGCCGCCAGGCATTGACAAAGTTCCGG 1131
Db 61 TGGGTGGCAACAATTCAGCTGATGACGATATGGCAGACCTGGCATTGAGAAGTTCCGA 120

QY 1132 GAGGAGCCCTTAAGAGGAGACATCTGATTTGACTTCAGTGAGATGATCTCTCAGTACTAC 1191
Db 121 GAGGAAGCCGAAGAGAGGATATCTGCAATTTAGCGAGCTCATCTCCAGTACTCT 180

QY 1192 ACCCAGAAAGCAGTTGGAGTTTCATCGCCGAGCTCATCCAGAACTCTCTCGGCCAAGTCATC 1251
Db 181 GACGAGGAAGAGATCCAGCAGAGTGGTTCGAAGTGATCCAAAACCTCTACGCCAAGGTCATT 240

QY 1252 GTGGTCTTCTCCATGGCCCGGACCTGGAGCCGCTCATCCAGGAGATAGTTTCGGAGAAC 1311
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QY 1312 ATCACCAGATCGGATCTGGCTGGCCAGCGAGCTTGGCCAGCTCTTCGCTCATTTGCCAAG 1371
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QY 1372 CCAGAGTACTTCCAGCTGGTGGCGGACCATCGGCTTGGCTCTCAGGGGGGGCGGTATC 1431
Db 361 CCTGAGTATTTCCATGTAGTGGGGGACCATTTGGGTTTCGGTCTGAAGCTCGGCGAGATT 420

QY 1432 CCAGGTTCAACAAGTTCTCTGAAGAGAGTCCACCCAGCAGAGTCTCTCGGACATGGGTTT 1491
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QY 1492 GTCAAGAGGTTCTGGAGGAGACCTTTCAACTGCTACTTCCCGAGAGAACCTTCAGCGAG 1551
Db 481 GCCAAAGAGTTTGGGAAGAAACTTTTAAATTTGCCAC--CTCCAAAGAGGCGCAAAAGGAC 538

QY 1552 CTGAAGAAATTCGAAGTGGCTTCGACGAGACCGCGGCTCAGGGGACCGCTCCAGGGG 1611
Db 539 CTTTACCTGAGGACACTTCGTGAGAG--TCACGAAGAGGTGGCAACAGG 588

QY 1612 GGGAACTCCAGAGCGAGACGCTTACGCCACCCCTGCACTGGGAGGAGAACATCACCAGC 1671
Db 589 TTACTCAATAGCTCTACTGCTTCCGACCCCTCTGCAAGGGGATGAGAATCAACACT 648

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QY 1732 GTCTACTCTCACTGCTCAGCCCTTGCAGAGACATCCACTCTTGTCAAAACCCGCGC 1782

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Db 706 GCTACTCTTTGGCATGCCACAGATATACCCCTGCTACCGGAGAGGC 756

RESULT 15  
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 LOCUS  
 DEFINITION  
 BB615658 RIKEN full-length enriched, adult male testis Mus musculus  
 cDNA clone 4930542118 5', mRNA sequence.  
 BB615658  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 BB615658.1 GI:16455904  
 EST.  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 653)  
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,  
 Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,  
 Konno, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, K., Nomura, K.,  
 Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
 Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
 Unpublished (2001)  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,  
 Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.  
 and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,  
 Sugahara, Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,  
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
 Hayashizaki, Y.  
 Computational Analysis of Full-length Mouse cDNAs Compared with  
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for  
 further details.  
 e mouse tissues.  
 Location/Qualifiers  
 1. .653  
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 Project of Genome Exploration Research Group in Riken

ORIGIN

Query Match 7.6%; Score 313.8; DB 2; Length 653;  
 Best Local Similarity 69.3%; Pred. No. 4e-59;  
 Matches 461; Conservative 0; Mismatches 192; Indels 12; Gaps 2;

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 Db 1 GAGGCTTGGCCAGCTCTTCGCTCATTCGACGAGAGTCTTCCACGCTGGCGCGC 60  
 Oy 1399 ACCATGGCTTCGCTCTCAGGGGGGGGGGCTATCCAGGGTTCACCAAGTTCCTGAAGGAG 1458  
 Db 61 ACCATGGGTTGGTTCGCTTCGAGGGTGGCAGATTCGAGGCTTCGAGAAATTCCTACAGAA 120  
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 Oy 1519 AACTGCTACTTACCCGAGAGAGCCCTGACGCGAGCTGAGAAATTCCAAGGTGCCTCGCAC 1578  
 Db 181 AATTGC-----CACCTGCAAGACGGCGCAAAAGAGACCTTTACCCGTGGACACCTTCGTGA 235  
 Oy 1579 GGACCGCGGCTCAAGGGGACGGCTCCAAAGCGGGGAACTCCACAGCGGACAGCCTACGC 1638  
 Db 236 GAA-----GTCAAGGAGGCGGCAACAGGTTACTCAATAGCTCCACTGCCTCCGA 288  
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 Db 289 CCCTCTGCACGGGGATGAAACATCAATAGTGTGAGACCCCTTACATGGACTACGAA 348  
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 Db 409 GATATATACACTGCTTACCCGGAAGAGGGCTTTTCAACCAACGGGCTCTGTGAGACATC 468  
 Oy 1819 AAAAAAGTTGAGCGCTGGCAGGTCCTCAACCATCTGCTGATCTGAAGTTTACCAACAGC 1878  
 Db 469 AAGAAGTTTGAGCGCTGGCAGGTCCTGAACACCTACGGCACCTGAATTTACCAACAC 528  
 Oy 1879 ATGGGTGAGCAGGTTGACCTTTGACGATCAAGGTGACCTCAAGGGGAACTACACATTATC 1938  
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 Db 649 GTGTA 653

Search completed: November 17, 2004, 06:55:13  
 Job time : 11890 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2004, 06:55:29 ; Search time 297 Seconds

(without alignments)  
1240.455 Million cell updates/sec

Title: US-10-016-496-2

Perfect score: 5410

Sequence: 1 MAQLHCQLFLGFTLLQSYN.....KGTLESPGSKERTTMEET 1027

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_23Sep04:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5410	100.0	1027	AAU76004	Shark kid
2	5410	100.0	1027	ABW78761	Dogfish s
3	5410	100.0	1027	ADH10917	Shark pol
4	5410	100.0	1027	ABW02706	Dogfish s
5	5410	100.0	1027	ADI19970	Dogfish s
6	5251.5	97.1	1026	AAW32059	Dogfish s
7	4106.5	75.9	1059	AAU00508	Chicken c
8	4055.5	75.0	1078	AAU02195	Cynomolgo
9	4044.5	74.8	1078	AAU70325	Human wil
10	4044.5	74.8	1078	ADD48571	Human Pro
11	4044.5	74.8	1078	AD621143	Human Pro
12	4044.5	74.8	1078	AD621147	Human Pro
13	4044.5	74.8	1078	ADH10955	Human par
14	4044.5	74.8	1078	ADJ68365	Human hea
15	4044.5	74.8	1078	ADI41014	Human GPC
16	4044.5	74.8	1078	ADI40962	Human GPC
17	4044.5	74.8	1078	ADO29211	Human GPC
18	4039.5	74.7	1078	ADJ93192	Human ext
19	4039.5	74.7	1078	ABG72193	Human cal
20	4037.5	74.6	1078	AAW11889	Parathyro
21	4037.5	74.6	1078	AAW54846	Human par
22	4037.5	74.6	1078	AAW38274	Human par
23	4037.5	74.6	1078	AAW28840	Human cal
24	4037.5	74.6	1078	AAW41780	Human par
25	4037.5	74.6	1078	AAW89565	Human par

26	4037.5	74.6	1078	3	AAV51827	Human cal
27	4037.5	74.6	1078	4	AAW74391	Protein e
28	4037.5	74.6	1078	5	AAW47822	HuCar4.0.
29	4037.5	74.6	1078	6	ABP81817	Human cal
30	4029.5	74.5	1088	2	AAW11888	Parathyro
31	4029.5	74.5	1088	2	AAW54845	Human par
32	4029.5	74.5	1088	2	AAW41779	Human par
33	4029.5	74.5	1088	2	AAW89564	Human par
34	4029.5	74.5	1088	3	AAV51826	Human cal
35	4029.5	74.5	1088	4	AAW74390	Protein e
36	4029.5	74.5	1088	5	AAW47821	HuPCAR5.2
37	4029.5	74.5	1088	8	ADW47114	Human cal
38	4029.5	74.5	1089	7	ADD48589	Human pro
39	4022.5	74.4	1088	2	AAW38273	Human par
40	3999.5	73.9	1085	2	AAW54844	Bovine pa
41	3999.5	73.9	1085	2	AAW38272	Bovine pa
42	3999.5	73.9	1085	2	AAW41778	Bovine pa
43	3999.5	73.9	1085	2	AAW89563	Bovine pa
44	3999.5	73.9	1085	3	AAV51825	Bovine ca
45	3999.5	73.9	1085	5	AAW47820	BoPCAR1.

ALIGNMENTS

RESULT 1  
AAU76004  
ID AAU76004 standard; protein; 1027 AA.  
XX AC AAU76004;  
XX DT 07-AUG-2003 (revised)  
DT 08-MAY-2002 (first entry)  
XX DE Shark kidney calcium receptor related protein-1 (SKCar-RP-1).  
XX KW Shark kidney calcium receptor related protein-1; SKCar-RP-1;  
KW polyvalent cation-sensing receptor protein; PVCR; fish; flounder;  
KW salinity tolerance; fat content; protein content; weight;  
KW fish maturation; fish development; spiny dogfish.  
XX OS Squalus acanthias.  
XX FN US6337391-B1.  
XX PD 08-JAN-2002.  
XX PF 28-SEP-1998; 98US-00162021.  
XX PR 27-MAR-1996; 96US-00622738.  
XX PR 27-MAR-1997; 97WO-US005031.  
XX PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
XX PI Harris HW, Brown EM, Hebert SC;  
XX WPI; 2002-163246/21.  
XX DR N-PSDB; ABK14910.  
XX PT New nucleic acid molecule encoding polyvalent cation-sensing receptor protein, useful for regulating adaptation of fish e.g. flounder to marine and fresh water environments, and to alter tissue or meat/muscle composition.  
XX PS Claim 4; Fig 5A-E; 83pp; English.  
XX CC The invention describes an isolated nucleic acid sequence (I) encoding a polyvalent cation-sensing receptor protein (PVCR), especially Shark Kidney calcium receptor related protein-I (SKCar-RP-I) that allows fish to sense ion concentrations. The aquatic PVCR allows the successful adaptation of fish, such as flounder, to marine and fresh water environments, and controls maturation and developmental stages in marine species. Modulating the expression of PVCR activates or inhibits PVCR

CC	mediated ion transport and endocrine changes that permit fish to adapt to
CC	fresh or salt water. Activating pVCR in epithelial cells increases or
CC	decreases salinity tolerance in aquatic species. Regulating salinity
CC	tolerance is useful to develop new species of marine fish that are easily
CC	adaptable to fresh water aqua culture. The methods are useful for:
CC	altering body composition e.g. fat content, protein content, weight,
CC	thickness, moisture and taste. The species can be maintained in both
CC	environments, consecutively to reduce parasites, bacteria and
CC	contaminants. This is the amino acid sequence of the shark kidney calcium
CC	receptor related protein-1 (SKCaR-pp-1), described in the method of the
CC	invention. (Updated on 07-AUG-2003 to correct OS field.)
XX	
SQ	Sequence 1027 AA;
Query Match	100.0%; Score 5410; DB 5; Length 1027;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1027; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MAQLHCQLLFLGFTLLQSNVSGYGNPQRAQKKGDIILGGLFPIHFGVAAKQDQLKSRPE 60
Db	1 MAQLHCQLLFLGFTLLQSNVSGYGNPQRAQKKGDIILGGLFPIHFGVAAKQDQLKSRPE 60
Qy	61 ATKCIYRNPGRFQWQAMIFAEIENNSMTFLPNITLGVRIPTDCTNTVSKALEATLSFVA 120
Db	61 ATKCIYRNPGRFQWQAMIFAEIENNSMTFLPNITLGVRIPTDCTNTVSKALEATLSFVA 120
Qy	121 QNKIDSLNLDLFCNCSHDHPSIAVVGATGSGISTAVANLLGLFYIPOVSVASSRLLSN 180
Db	121 QNKIDSLNLDLFCNCSHDHPSIAVVGATGSGISTAVANLLGLFYIPOVSVASSRLLSN 180
Qy	181 KNEYKAFILTIENDEQQAAMAEIIEHFQWNVGTLAADDYGRGIDKFRFEAVKRDIC 240
Db	181 KNEYKAFILTIENDEQQAAMAEIIEHFQWNVGTLAADDYGRGIDKFRFEAVKRDIC 240
Qy	241 IDPSEMSIYQTKOLEFTADVIQNSSAKVIVFNSGPDLEPLIOEIVRMTIDRIWLAS 300
Db	241 IDPSEMSIYQTKOLEFTADVIQNSSAKVIVFNSGPDLEPLIOEIVRMTIDRIWLAS 300
Qy	301 EAWASSLLIAKPEYFHVVGTTGFALRAGRIFGFNKFLKEVHPSRSSNGFVKPEWETP 360
Db	301 EAWASSLLIAKPEYFHVVGTTGFALRAGRIFGFNKFLKEVHPSRSSNGFVKPEWETP 360
Qy	361 NCYFTEKTLTQKNSKVPBGHGAAGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420
Db	361 NCYFTEKTLTQKNSKVPBGHGAAGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420
Qy	421 HLRISYVAVVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAWQVNLHLHLKFTNS 480
Db	421 HLRISYVAVVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAWQVNLHLHLKFTNS 480
Qy	481 MGEQVDFDDGGDLKGNVTIINWOLSNEDSVLFHEVGNVAYAKPSDRNLNKKILMSG 540
Db	481 MGEQVDFDDGGDLKGNVTIINWOLSNEDSVLFHEVGNVAYAKPSDRNLNKKILMSG 540
Qy	541 FSKVVPFNSCRDPCVPGTRKGIIEGEPTCCFECMACAEFSDENDASACTKCPNDFWSN 600
Db	541 FSKVVPFNSCRDPCVPGTRKGIIEGEPTCCFECMACAEFSDENDASACTKCPNDFWSN 600
Qy	601 ENHTSCIAKEIYLSWTEPFGIALTIFAVLGLITTSFVLGVFIKRPNTPIVKATNRELVS 660
Db	601 ENHTSCIAKEIYLSWTEPFGIALTIFAVLGLITTSFVLGVFIKRPNTPIVKATNRELVS 660
Qy	661 LLLFSLICCFSSSLFIPIGPRDWTCLROPAGISFVLCISILVKNRVLVPEAKIPT 720
Db	661 LLLFSLICCFSSSLFIPIGPRDWTCLROPAGISFVLCISILVKNRVLVPEAKIPT 720
Qy	721 SLHRKWVGNLQFLVFLCILVQIVTCIWLVTAPPPSSYRNHLESDVIFITCDEGSLMA 780
Db	721 SLHRKWVGNLQFLVFLCILVQIVTCIWLVTAPPPSSYRNHLESDVIFITCDEGSLMA 780
Qy	781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFTTFSMLIFFIWIWISFIPAYVSTYKGF 840
Db	781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFTTFSMLIFFIWIWISFIPAYVSTYKGF 840

Qy	841 VSAVEVIAILASSFGLLGCIFYFNKCVIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
Db	841 VSAVEVIAILASSFGLLGCIFYFNKCVIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
Qy	901 AASRKSSSLCCSTISSPASSTCGPLTMMQRCSTQKVSFGSGTIVTSLSTEETGRYAT 960
Db	901 AASRKSSSLCCSTISSPASSTCGPLTMMQRCSTQKVSFGSGTIVTSLSTEETGRYAT 960
Qy	961 LSTARSNSADGRSGDDLPSRHHDDGPPQKCEPQANDARYKAAPTKGTLSPPGSKER 1020
Db	961 LSTARSNSADGRSGDDLPSRHHDDGPPQKCEPQANDARYKAAPTKGTLSPPGSKER 1020
Qy	1021 PTTMEET 1027
Db	1021 PTTMEET 1027
RESULT 2	
ABB78761	
ID	ABB78761 standard; protein; 1027 AA.
XX	
AC	ABB78761;
XX	
DT	23-JUL-2002 (first entry)
XX	
DE	Dogfish shark kidney cation receptor (SKCaR) protein SEQ ID NO:18.
XX	
KW	Fish; polyvalent cation sensing receptor; pVCR; anadromous fish;
KW	polyvalent cation sensing receptor modulator; pVCR modulator; feed;
KW	atlantic salmon; arctic char; rainbow trout.
XX	
OS	Squalus acanthias.
XX	
FN	WO200230182-A2.
XX	
PD	18-APR-2002.
XX	
PF	11-OCT-2001; 2001WO-US031562.
XX	
PR	12-OCT-2000; 2000US-00687372.
PR	12-OCT-2000; 2000US-00687476.
PR	12-OCT-2000; 2000US-00687477.
XX	
DA	(AQUA-) AQUABIO PROD SCI LLC.
XX	
FI	Harris WH, Russell DR, Nearing J, Betka M;
XX	
DR	WPI; 2002-416815/44.
DR	N-PSDB; ABL59964.
XX	
PT	Improving the raising of pre-adult anadromous fish e.g. salmon involves
PT	adding polyvalent cation sensing receptor modulator and a feed containing
PT	an agent that increases level of modulator in serum of fish.
PS	
XX	Example 1; Fig 28; 201pp; English.
XX	
CC	The present invention describes a method for improving the raising of pre
CC	-adult anadromous fish maintained in fresh water prior to transfer to
CC	seawater. The method involves: (a) adding at least one polyvalent cation
CC	sensing receptor (pVCR) modulator to the fresh water; and (b) adding a
CC	feed containing an agent that increases the level of pVCR modulator in
CC	the serum of fish. The pVCR modulator has anabolic activity. The method
CC	can be used for improving the raising of pre-adult anadromous fish e.g.
CC	salmon, char and trout, maintained in fresh water prior to transfer to
CC	seawater. The present sequence represents dogfish shark kidney cation
CC	receptor (SKCaR), which is relative to the pVCRs from salmon, char and
XX	trout
SQ	Sequence 1027 AA;
Query Match	100.0%; Score 5410; DB 5; Length 1027;
Best Local Similarity	100.0%; Pred. No. 0;

Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	MAQHCQLLFLGFTLLQSYNVSGYGNORAKKGGDIILGGLFPIHFGVAAKQDQKSRPE	60
Db	1	MAQHCQLLFLGFTLLQSYNVSGYGNORAKKGGDIILGGLFPIHFGVAAKQDQKSRPE	60
Qy	61	ATKCIYRNFGRFLQAMIFAEIEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA	120
Db	61	ATKCIYRNFGRFLQAMIFAEIEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA	120
Qy	121	QNKIDSLNLDLDFNCSDHIPSTIAVVGATGGISTAVANLLGLFYIPQVSYASSSRLSN	180
Db	121	QNKIDSLNLDLDFNCSDHIPSTIAVVGATGGISTAVANLLGLFYIPQVSYASSSRLSN	180
Qy	181	KNEYKAFRLTIPNDEQQATAMAEIIEHFQWNVGTLAADDYGRPGIDKFREEAVKRDIC	240
Db	181	KNEYKAFRLTIPNDEQQATAMAEIIEHFQWNVGTLAADDYGRPGIDKFREEAVKRDIC	240
Qy	241	IDFSEMSIQYTKQLEFIADVIQNSSAKVIVFNSNGFDLEPLIQEIVRRNITDRIWLAS	300
Db	241	IDFSEMSIQYTKQLEFIADVIQNSSAKVIVFNSNGFDLEPLIQEIVRRNITDRIWLAS	300
Qy	301	EAWASSSLIAKPEYHVUVGGTIGFALRAGRIPGKELKEVHPRSSDNGFVKEFWETP	360
Db	301	EAWASSSLIAKPEYHVUVGGTIGFALRAGRIPGKELKEVHPRSSDNGFVKEFWETP	360
Qy	361	NCYFTEKTLTQKNSKVPESHGPAAGQDGSKAGNSRRRTALRHPCCTGEENITSVETPYLDYT	420
Db	361	NCYFTEKTLTQKNSKVPESHGPAAGQDGSKAGNSRRRTALRHPCCTGEENITSVETPYLDYT	420
Qy	421	HLRISYNYVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVPAMQVNLHLLKFTNS	480
Db	421	HLRISYNYVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVPAMQVNLHLLKFTNS	480
Qy	481	MGEQVDFDDQDGLKGNYYTIINWQLSAEDSVLFEHVGNYNAYAKPSRLNINEKILWSG	540
Db	481	MGEQVDFDDQDGLKGNYYTIINWQLSAEDSVLFEHVGNYNAYAKPSRLNINEKILWSG	540
Qy	541	FSKVVPFNSCRDCVPGTRKGIIEGEPTCCPECACAEGEFSDENDASACTKCPNDFWSN	600
Db	541	FSKVVPFNSCRDCVPGTRKGIIEGEPTCCPECACAEGEFSDENDASACTKCPNDFWSN	600
Qy	601	ENHSCIAKEIYLSWTFPGFALTIFAVLGLITTSFVLGVFIKFRNTPIVKATNRELSY	660
Db	601	ENHSCIAKEIYLSWTFPGFALTIFAVLGLITTSFVLGVFIKFRNTPIVKATNRELSY	660
Qy	661	LLFSLICCFSSSLIFIGEPRDWTCLRQPAFGISFVLCISCLVKNRVLLVFEAKIPT	720
Db	661	LLFSLICCFSSSLIFIGEPRDWTCLRQPAFGISFVLCISCLVKNRVLLVFEAKIPT	720
Qy	721	SLHRKWVGLNQFLVFLCIIQIVTCTIWIYTAPPSSYRNHELEDEVIPTCDEGSIMA	780
Db	721	SLHRKWVGLNQFLVFLCIIQIVTCTIWIYTAPPSSYRNHELEDEVIPTCDEGSIMA	780
Qy	781	LGFLIGYTCLLAAICFFFAFKSRKLPENFNKAITTFMSLFFFIWISFIPAYVSTYCKP	840
Db	781	LGFLIGYTCLLAAICFFFAFKSRKLPENFNKAITTFMSLFFFIWISFIPAYVSTYCKP	840
Qy	841	VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS	900
Db	841	VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS	900
Qy	901	AASRRSSSLCGSTISSPASSTCGPLTMEQRCSTQKVSFGSGVTLSLFEETGRYAT	960
Db	901	AASRRSSSLCGSTISSPASSTCGPLTMEQRCSTQKVSFGSGVTLSLFEETGRYAT	960
Qy	961	LSRTARSNSADCRGDDLPSEHHDQGPQKCEPOPANDARYKKAAPTGTLESFGGSKER	1020
Db	961	LSRTARSNSADCRGDDLPSEHHDQGPQKCEPOPANDARYKKAAPTGTLESFGGSKER	1020
Qy	1021	PTTMEET 1027	
Db	1021	PTTMEET 1027	

RESULT 3

ADHI0917  
ID ADHI0917 standard; protein; 1027 AA.

XX ADHI0917;

XX AC AC

DT 11-MAR-2004 (first entry)

XX Shark polyvalent cation sensing receptor (PVCr)-related protein.

DE polyvalent cation sensing receptor; PVCr; shark; growth increase;

XX mortality reduction.

KW Unidentified.

OS Unidentified.

XX WO2003087331-A2.

PN 23-OCT-2003.

PD 09-APR-2003; 2003WO-US011188.

XX 11-APR-2002; 2002US-00121441.

PR 18-APR-2002; 2002US-00125772.

PR 18-APR-2002; 2002US-00125778.

PR 18-APR-2002; 2002US-00125792.

XX (MARI-) MARICAL INC.

XX Harris HW, Nearing J, Betka M;

PI WPI; 2003-845319/78.

XX N-PSDB; ADHI0916.

DR New Atlantic salmon polyvalent cation-sensing receptor, PVCr,

XX polypeptides useful in commercial raising of salmon and restoration of

PT wild Atlantic salmon populations especially in transfer from freshwater

PT to seawater.

XX Example 1; SEQ ID NO 2; 269pp; English.

XX The invention comprises the amino acid and coding sequences of polyvalent

CC cation sensing receptor (PVCr) proteins from Atlantic salmon. The DNA and

CC protein sequences of the invention are useful in the commercial raising

CC of Atlantic salmon and the restoration of wild Atlantic salmon

CC populations, especially in the transfer from freshwater to seawater with

CC increased growth and reduced mortality. The present amino acid sequence

CC represents a shark PVCr-related protein.

XX Query Match 100.0%; Score 5410; DB 7; Length 1027;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQHCQLLFLGFTLLQSYNVSGYGNORAKKGGDIILGGLFPIHFGVAAKQDQKSRPE 60

Db 1 MAQHCQLLFLGFTLLQSYNVSGYGNORAKKGGDIILGGLFPIHFGVAAKQDQKSRPE 60

Qy 61 ATKCIYRNFGRFLQAMIFAEIEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA 120

Db 61 ATKCIYRNFGRFLQAMIFAEIEINNSMTFLPNITLGYRIFDTCNTVSKALEATLSFVA 120

Qy 121 QNKIDSLNLDLDFNCSDHIPSTIAVVGATGGISTAVANLLGLFYIPQVSYASSSRLSN 180

Db 121 QNKIDSLNLDLDFNCSDHIPSTIAVVGATGGISTAVANLLGLFYIPQVSYASSSRLSN 180

Qy 181 KNEYKAFRLTIPNDEQQATAMAEIIEHFQWNVGTLAADDYGRPGIDKFREEAVKRDIC 240

Db 181 KNEYKAFRLTIPNDEQQATAMAEIIEHFQWNVGTLAADDYGRPGIDKFREEAVKRDIC 240

Qy 241 IDFSEMSIQYTKQLEFIADVIQNSSAKVIVFNSNGPDLEPLIQEIVRRNITDRIWLAS 300

	DB	241	IDFSEMI	SQY	TQKLEFIADVIQNSSAKVIVVNSGPDLEPLIQEIVRRNITDRIWLAS	300
	QY	301	EAWASSSLIAKPEY	FHVHVGGTIGFALRAGRIPGFNFKLKEVHPGRSSDNGVFKEFWBETP	360	
	DB	301	EAWASSSLIAKPEY	FHVHVGGTIGFALRAGRIPGFNFKLKEVHPGRSSDNGVFKEFWBETP	360	
	QY	361	KCYFTTEKTLTOLKNSKVESHGPAAAGDGDSKAGNSRRRTALRHPCTCGEENITSVEPYLDYT	420		
	DB	361	KCYFTTEKTLTOLKNSKVESHGPAAAGDGDSKAGNSRRRTALRHPCTCGEENITSVEPYLDYT	420		
	QY	421	HLRSINYNYVVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAQQVLNHLHLKFPNS	480		
	DB	421	HLRSINYNYVVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAQQVLNHLHLKFPNS	480		
	QY	481	MGEQVDPDFDDGLGNITYIIINQLSABDESVLFEHVGYNAYAKPSDELNTINEKKILWSG	540		
	DB	481	MGEQVDPDFDDGLGNITYIIINQLSABDESVLFEHVGYNAYAKPSDELNTINEKKILWSG	540		
	QY	541	FSKVVPFNSCNRDCVPGTRKGIIIEGPTCCFECKACAEGBESDENASACTKCPNDFSWN	600		
	DB	541	FSKVVPFNSCNRDCVPGTRKGIIIEGPTCCFECKACAEGBESDENASACTKCPNDFSWN	600		
	QY	601	ENHTSCIATKEIYLSWTBPPFGIALTIFAVLGILITSFVLGVFIKRPNTPIVKATNRELSY	660		
	DB	601	ENHTSCIATKEIYLSWTBPPFGIALTIFAVLGILITSFVLGVFIKRPNTPIVKATNRELSY	660		
	QY	661	LLLFSLICCFSSSLIFICEPRDWTCRLQPAGISFVLICISCLLVKTNRVLLVFEAKIPT	720		
	DB	661	LLLFSLICCFSSSLIFICEPRDWTCRLQPAGISFVLICISCLLVKTNRVLLVFEAKIPT	720		
	QY	721	SLHRKWGLNQFLVLVFLCILVQIVTCIIMLYTAPPSSYRNHELEDEVIFITCDEGSIMA	780		
	DB	721	SLHRKWGLNQFLVLVFLCILVQIVTCIIMLYTAPPSSYRNHELEDEVIFITCDEGSIMA	780		
	QY	781	LGFVLGYTCLLAAACFFFAFKSRKLPENFNKAFTTFSMLIFFFIWISFIPAYVSTYCKP	840		
	DB	781	LGFVLGYTCLLAAACFFFAFKSRKLPENFNKAFTTFSMLIFFFIWISFIPAYVSTYCKP	840		
	QY	841	VSAVEVIAILASSFGLLCGIYFNKCYYIILFKPCRNITBEVRCSTAHAHFKAARATLRSS	900		
	DB	841	VSAVEVIAILASSFGLLCGIYFNKCYYIILFKPCRNITBEVRCSTAHAHFKAARATLRSS	900		
	QY	901	AASRKSSSLCGSTISSPASCTCGELTMEXQRCSQKVSFGSGVTLSLSFEETGRYAT	960		
	DB	901	AASRKSSSLCGSTISSPASCTCGELTMEXQRCSQKVSFGSGVTLSLSFEETGRYAT	960		
	QY	961	LSRTARGSNSADGRSGDDLPSRHHDDQGPFQPKCEQPANDARYKAAPTGTLTLESFGGSKER	1020		
	DB	961	LSRTARGSNSADGRSGDDLPSRHHDDQGPFQPKCEQPANDARYKAAPTGTLTLESFGGSKER	1020		
	QY	1021	PTTWEEET	1027		
	DB	1021	PTTWEEET	1027		

RESULT 4  
 AEW02706  
 ID AEW02706 standard; protein; 1027 AA.  
 XX AC AEW02706;  
 XX DT 11-MAR-2004 (first entry)

XX	04-SEP-2003.	
XX		
XX	10-DEC-2001; 2001US-00016496.	
XX		
XX	27-MAR-1996; 96US-00622738.	
XX	27-MAR-1997; 97WO-US005031.	
XX	28-SEP-1998; 98US-00162021.	
XX	17-NOV-2000; 2000US-00715538.	
XX		
PA	(EGHM ) BRIGHAM & WOMENS HOSPITAL.	
XX		
PI	Harris HW, Brown EM, Hebert SC;	
XX		
DR	WPI; 2003-874926/81.	
DR	N-PSDB; AAD64738.	
XX		
XX	Fish polyvalent cation-sensing receptor proteins, useful for assisting	
PT	fish in adapting to changing ion concentrations by altering water intake	
PT	and absorption, urine output or for modulating the fat, protein and	
PT	moisture content of muscle.	
XX		
XX	Claim 7; SEQ ID NO 2; Opp; English.	
PS		
XX		
CC	The invention relates to aquatic polyvalent cation-sensing receptor	
CC	(PVCRI) proteins and methods of regulating PVCRI functions in aquatic	
CC	species. PVCRI is used to screen candidate compounds that may be used to	
CC	assist fish in adapting to changing ion concentrations by altering water	
CC	intake, water absorption or urine output and/or for modulating the	
CC	percentage of total fat, protein and moisture of muscle of the fish. The	
CC	present sequence is dogfish shark kidney calcium receptor related protein	
CC	-I (SKCAR-RP-I or SKCAR-I). This sequence is used to illustrate the	
CC	method of the invention	
XX		
XX	Sequence 1027 AA;	
SQ		
	Query Match 100.0%; Score 5410; DB 7; Length 1027;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

RESULT 4  
ABW02706

ID ABW02706 standard: protein: 1027 AA.

AC ABW02706:

XXXX

— 222 —

DE . Dogfish shark kidney calcium

KW Polyvalent cation-sensing receptor; pVCR; anabolic; homeostatic;

KW shark kidney calcium receptor related protein-I; SKCaR-RP-I;

XX

OS Squalas acanthias.

PN US2003166908-A1.

Db 481 MGEQVDFDDQDGLKGNYYIIINWQLSAEDESVLFEHVGNNAYAKPSDELNINEKKILWSG 540  
Qy 541 FSKVVPFNSGRDCVPGTRKGIIEGEPTCCPECACAESESDNDASACTKCPNDPWSN 600  
Db 541 FSKVVPFNSGRDCVPGTRKGIIEGEPTCCPECACAESESDNDASACTKCPNDPWSN 600  
Qy 601 ENHTSCIAKEIEYLSWTFPGIALTIPAVLGILITTSFVLGVFIKFRNTPIVKATNRELSY 660  
Db 601 ENHTSCIAKEIEYLSWTFPGIALTIPAVLGILITTSFVLGVFIKFRNTPIVKATNRELSY 660  
Qy 661 LLLFSLICCFSSSLIFIGEPRDWTCLRQPAFGISFVLCISCLVKNRVLVFEAKIPT 720  
Db 661 LLLFSLICCFSSSLIFIGEPRDWTCLRQPAFGISFVLCISCLVKNRVLVFEAKIPT 720  
Qy 721 SLHRKWGLNQFLVFLCIIIVQVTCIIWLYTAPSSYRNHELEDEVIPTCDEGSLMA 780  
Db 721 SLHRKWGLNQFLVFLCIIIVQVTCIIWLYTAPSSYRNHELEDEVIPTCDEGSLMA 780  
Qy 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNFAKFTTFMSLIIFFIIVWISFIPAYVSTYKGF 840  
Db 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNFAKFTTFMSLIIFFIIVWISFIPAYVSTYKGF 840  
Qy 841 VSAVEVIAILASSFGLLCIYFNKCYIILFKPCRNTEIEEVRCSAAHAFKVAARATLRS 900  
Db 841 VSAVEVIAILASSFGLLCIYFNKCYIILFKPCRNTEIEEVRCSAAHAFKVAARATLRS 900  
Qy 901 AASRXPSSLCGSTISSPASSTCGPLTWEMQRCSTQKVSFGSGVTLLSLFEETGRYAT 960  
Db 901 AASRXPSSLCGSTISSPASSTCGPLTWEMQRCSTQKVSFGSGVTLLSLFEETGRYAT 960  
Qy 961 LSRTARSNSADGRGDDLPGRHHDQPPQKCEPOPANDARYKAAPTKGTLESPPGSKER 1020  
Db 961 LSRTARSNSADGRGDDLPGRHHDQPPQKCEPOPANDARYKAAPTKGTLESPPGSKER 1020  
Qy 1021 PTTMEET 1027  
Db 1021 PTTMEET 1027

RESULT 5  
ADI19970  
ID ADI19970 standard; protein; 1027 AA.  
XX ADI19970;  
AC ADI19970;  
DT 15-APR-2004 (first entry)  
XX Dogfish shark kidney cation receptor (SKCar) protein.  
DE Pre-adult anadromous fish; polyvalent cation sensing receptor; PVCR;  
KW stress; dogfish shark; receptor.  
XX Squalus acanthias.  
OS US2003230247-A1.  
XX 18-DEC-2003.  
XX 09-APR-2003; 2003US-00410872.  
XX 12-OCT-2000; 2000US-00687372.  
XX 12-OCT-2000; 2000US-00687476.  
XX 12-OCT-2000; 2000US-00687477.  
XX 11-OCT-2001; 2001US-00975553.  
XX 11-OCT-2001; 2001WO-US031562.  
XX (MARI-) MARICAL INC.  
XX Harris HW, Russell DR, Nearing J, Betka M;  
XX WPI; 2004-061122/06.  
XX N-PSDB; ADI19962.

XX Growing pre-adult anadromous fish in freshwater comprises adding feed  
PT containing an amount of NaCl for fish consumption to the freshwater to  
PT increase the level of the Polyvalent Cation Sensing Receptor modulator in  
PT serum of the fish.  
XX  
PS Example 19; Fig 28; 109pp; English.  
XX The present invention relates to methods for improving the raising of pre  
CC -adult anadromous fish or preparing these fish for transfer to seawater  
CC by modulating expression of a receptor referred to as the Polyvalent  
CC Cation Sensing Receptor (PVCR). The invention is useful in increasing  
CC survival and growth and reduce stress of the fish that have been  
CC transferred to seawater. The present sequence is a dogfish shark cation  
CC receptor (SKCar) protein.  
XX  
SQ Sequence 1027 AA;  
Query Match 100.0%; Score 5410; DB 8; Length 1027;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAQLHCOLLPLGFTLLQSYNVSGYGNQRAQKKGDIILGGLPFIHFGVAAKQDQLSRPE 60  
Db 1 MAQLHCOLLPLGFTLLQSYNVSGYGNQRAQKKGDIILGGLPFIHFGVAAKQDQLSRPE 60  
Qy 61 ATKIRYNFRGPRWLQAMIFAEIEINNSMTFLPNITLGYRIPTDCTNTVSKALEATLSFVA 120  
Db 61 ATKIRYNFRGPRWLQAMIFAEIEINNSMTFLPNITLGYRIPTDCTNTVSKALEATLSFVA 120  
Qy 121 QNKIDSLNLDNFCNCDHIPSTIIVVVGATGSGISTAVANLLGLFYIPOVSYASSSLLSN 180  
Db 121 QNKIDSLNLDNFCNCDHIPSTIIVVVGATGSGISTAVANLLGLFYIPOVSYASSSLLSN 180  
Qy 181 KNEYKAFRLTIPNDEQOQATAMABIEHFQWNVWVGTAAADDDYGRPGIDKFRFEAVKRDIC 240  
Db 181 KNEYKAFRLTIPNDEQOQATAMABIEHFQWNVWVGTAAADDDYGRPGIDKFRFEAVKRDIC 240  
Qy 241 IDFSEMSIQYTKOLEFTADVIQNSAKVIVVFSNGPDLEPLIQIQRNITDRIWLAS 300  
Db 241 IDFSEMSIQYTKOLEFTADVIQNSAKVIVVFSNGPDLEPLIQIQRNITDRIWLAS 300  
Qy 301 EAWASSLLAKPEYFHVVGTTIGFALRAGRIPOGFKLKEVHPSRSDNGFVKEFEET 360  
Db 301 EAWASSLLAKPEYFHVVGTTIGFALRAGRIPOGFKLKEVHPSRSDNGFVKEFEET 360  
Qy 361 NCYFTEKTLTQLXNSKVPSPHGAQDGGKAGNSRRRTALRHPCTGSENITSVETPYLDYT 420  
Db 361 NCYFTEKTLTQLXNSKVPSPHGAQDGGKAGNSRRRTALRHPCTGSENITSVETPYLDYT 420  
Qy 421 HLRISVNVVAVYSIAHALQDIHSCXPGTGI FANGSCADIKKYEAQVNLHLHLKFTNS 480  
Db 421 HLRISVNVVAVYSIAHALQDIHSCXPGTGI FANGSCADIKKYEAQVNLHLHLKFTNS 480  
Qy 481 MGEQVDFDDQDGLKGNYYIIINWQLSAEDESVLFEHVGNNAYAKPSDRNLNINEKKILWSG 540  
Db 481 MGEQVDFDDQDGLKGNYYIIINWQLSAEDESVLFEHVGNNAYAKPSDRNLNINEKKILWSG 540  
Qy 541 FSKVVPFNSGRDCVPGTRKGIIEGEPTCCPECACAESESDNDASACTKCPNDPWSN 600  
Db 541 FSKVVPFNSGRDCVPGTRKGIIEGEPTCCPECACAESESDNDASACTKCPNDPWSN 600  
Qy 601 ENHTSCIAKEIEYLSWTFPGIALTIPAVLGILITTSFVLGVFIKFRNTPIVKATNRELSY 660  
Db 601 ENHTSCIAKEIEYLSWTFPGIALTIPAVLGILITTSFVLGVFIKFRNTPIVKATNRELSY 660  
Qy 661 LLLFSLICCFSSSLIFIGEPRDWTCLRQPAFGISFVLCISCLVKNRVLVFEAKIPT 720  
Db 661 LLLFSLICCFSSSLIFIGEPRDWTCLRQPAFGISFVLCISCLVKNRVLVFEAKIPT 720  
Qy 721 SLHRKWGLNQFLVFLCIIIVQVTCIIWLYTAPSSYRNHELEDEVIPTCDEGSLMA 780  
Db 721 SLHRKWGLNQFLVFLCIIIVQVTCIIWLYTAPSSYRNHELEDEVIPTCDEGSLMA 780

QY 781 LGFLIGYTCLLAACFFFAFKSRKLPENFNEAKPTFMSMLFFIIVWISFIPAYVSTYQKF 840  
 DB 781 LGFLIGYTCLLAACFFFAFKSRKLPENFNEAKPTFMSMLFFIIVWISFIPAYVSTYQKF 840  
 QY 841 VSAVEVIALASSFGLGCIYFNKCVIILFKPCRTNIEEVRCSAAHAFKVAARATLRRS 900  
 DB 841 VSAVEVIALASSFGLGCIYFNKCVIILFKPCRTNIEEVRCSAAHAFKVAARATLRRS 900  
 QY 901 AASRKRSSSLCGSTISSPASSSTCGPLTWMQRCSTQKVSFGSGTVTLISLFEETGRYAT 960  
 DB 901 AASRKRSSSLCGSTISSPASSSTCGPLTWMQRCSTQKVSFGSGTVTLISLFEETGRYAT 960  
 QY 961 LSRTARSNSADGRSGDDLPSSRHDDGPPQKCEPOPANDARYKAAPTKGTLESPPGSKER 1020  
 DB 961 LSRTARSNSADGRSGDDLPSSRHDDGPPQKCEPOPANDARYKAAPTKGTLESPPGSKER 1020  
 QY 1021 PTTMEET 1027  
 DB 1021 PTTMEET 1027  
 RESULT 6  
 AAW32059  
 ID AAW32059 standard; protein; 1026 AA.  
 AC AAW32059;  
 XX  
 DT 27-MAR-1998 (first entry)  
 XX  
 DE Dogfish shark kidney calcium receptor related protein (SKCar-RP).  
 XX  
 KW Calcium receptor related protein; Car-RP; dogfish shark; SKCar-RP;  
 KW polycation-sensing receptor; aquaculture; fish farming;  
 KW salinity tolerance.  
 XX  
 OS Squalus acanthias.  
 XX  
 FH Key  
 FT Region 351..395  
 FT /note= "region in extracellular domain that is highly  
 FT divergent from mammalian pVCR"  
 FT 870  
 FT Region  
 FT /note= "region in C-terminal domain that is highly  
 FT divergent from mammalian pVCR"  
 XX  
 PN WO9735977-A1.  
 XX  
 PD 02-OCT-1997.  
 XX  
 PF 27-MAR-1997; 97WO-US005031.  
 XX  
 PR 27-MAR-1996; 96US-00622738.  
 XX  
 PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 XX  
 PI Harris HW, Brown E, Hebert S;  
 DR WPI; 1997-489640/45.  
 DR N-P8DB; AAT89290.  
 XX  
 PT New isolated Aquatic polyvalent cation-sensing receptor - used to develop  
 PT products for increasing or decreasing the salinity tolerance of fish for  
 PT use in aquaculture.  
 XX  
 PS Claim 9; Fig 5A-B; 57pp; English.  
 XX  
 CC This protein comprises dogfish shark kidney calcium receptor related  
 CC protein (SKCar-RP), an aquatic polyvalent cation-sensing receptor (pVCR).  
 CC Its amino acid sequence was deduced from a kidney cDNA clone (see  
 CC AAT89290). It shows 74% homology to rat kidney pVCR and bovine  
 CC parathyroid pVCR and possesses general features that are homologous to  
 CC pVCR proteins, including a large extracellular domain, 7 transmembrane

CC domains and a cytoplasmic C-terminal domain. Also claimed are: an  
 CC isolated pVCR present in the plasma membranes of aquatic species,  
 CC especially on the apical membrane of epithelial cells of elasmobranch  
 CC fish, particularly from cells found in the collecting duct or late distal  
 CC tubule in the kidney, intestine, gill, rectal gland, gonad or brain; an  
 CC antibody that specifically binds to a pVCR; and a method of screening for  
 CC aquatic pVCR agonists and antagonists. Modulation of the expression of  
 CC the aquatic pVCR activates or inhibits aquatic pVCR mediated ion  
 CC transport and endocrine changes that permit fish to adapt to fresh or  
 CC salt water. The method facilitates the aquaculture of marine fish and can  
 CC provide for the development of marine fish that are easily adaptable to  
 CC fresh water aquaculture  
 XX  
 SQ Sequence 1026 AA;  
 Query Match 97.1%; Score 5251.5; DB 2; Length 1026;  
 Best Local Similarity 97.2%; Pred. No. 0;  
 Matches 1006; Conservative 1; Mismatches 11; Indels 17; Gaps 2;  
 QY 1 MAQLHCQLLFLGFTLLQSYNVSQYGNQRAQKGDIIILGGLPIHFGVAAKQDLKSRPE 60  
 DB 1 MAQLHCQLLFLGFTLLQSYNVSQYGNQRAQKGDIIILGGLPIHFGVAAKQDLKSRPE 60  
 QY 61 ATTCIRYNFRGFRWLQAMIFAEIINNMTFIPNITLGYRIIDTCTNTVSKALEATLSFVA 120  
 DB 61 ATTCIRYNFRGFRWLQAMIFAEIINNMTFIPNITLGYRIIDTCTNTVSKALEATLSFVA 120  
 QY 121 QNKIDSINLDEFCNSDHPSTIAVVGATSGISTAVANLLGLFYIPOVSYASSRSLSN 180  
 DB 121 QNKIDSINLDEFCNSDHPSTIAVVGATSGISTAVANLLGLFYIPOVSYASSRSLSN 180  
 QY 181 KNEYKAFIARTIPNDEQQAAMAEIIEHFQWNVVGTLLAADDYGRGIDKFREEAVKRDIC 240  
 DB 181 KNEYKAFIARTIPNDEQQAAMAEIIEHFQWNVVGTLLAADDYGRGIDKFREEAVKRDIC 240  
 QY 241 IDSEMIQYITQKOLEFIADVIQNSAKVIVFNSGPDLEPIQEIIVERNITDRIWLAS 300  
 DB 241 IDSEMIQYITQKOLEFIADVIQNSAKVIVFNSGPDLEPIQEIIVERNITDRIWLAS 300  
 QY 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIIPGNKFLKEVHP-----SRSSDNGFV 352  
 DB 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIIPGNKFLKEVHPAGRTWGLSRSSG---- 356  
 QY 353 KEFWSTFCYFTEKTLTOLKNSKVPSPHGAQGDGSKAGNSRRTALRHPCTGEENITSV 412  
 DB 357 -----RRLQLLHREDLTQLKNSKVPSHGPAAGDGSKAGNSRRTALRHPCTGEENITSV 411  
 QY 413 ETPYLDYTHLRISYNNVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAWOVLAHL 472  
 DB 412 ETPYLDYTHLRISYNNVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAWOVLAHL 471  
 QY 473 LHLKFTNSMGEQVDFDDQDGLKGNVTIINWQSADESVLFEVGNYNAYAKPSORLIN 532  
 DB 472 LHLKFTNSMGEQVDFDDQDGLKGNVTIINWQSADESVLFEVGNYNAYAKPSORLIN 531  
 QY 533 EKKILMSGSKVVPFNSCRDQVPGTRKGIIEGPTCCFECWACAGFESDNDASACTK 592  
 DB 532 EKKILMSGSKVVPFNSCRDQVPGTRKGIIEGPTCCFECWACAGFESDNDASACTK 591  
 QY 593 CPNDFWSNENHTSCIAKEIEYLSWTPEFGIALTIFAVLGILITSFVLGVFIKFRNTPIVK 652  
 DB 592 CPNDFWSNENHTSCIAKEIEYLSWTPEFGIALTIFAVLGILITSFVLGVFIKFRNTPIVK 651  
 QY 653 ATNRELSYLLLSLICPFSSSLIFIGEPDRDWTCLRQAPAGFISVLICISLIIVKNRVL 712  
 DB 652 ATNRELSYLLLSLICPFSSSLIFIGEPDRDWTCLRQAPAGFISVLICISLIIVKNRVL 711  
 QY 713 VFBAKPTSLHRKWGLNQLQFLVLCILVQIVTICIIWLYTAPPSSYRNHELEDEVIPT 772  
 DB 712 VFBAKPTSLHRKWGLNQLQFLVLCILVQIVTICIIWLYTAPPSSYRNHELEDEVIPT 771  
 QY 773 CDGSGSLMALGFLIGYTCLLAACFFFAFKSRKLPENFNEAKPTFMSMLFFIIVWISFIP 832



Db	772	CDEGLMALGFLIGVTCILAAICFFAFKSRKLPENFNEAKFITFMSLFIIVWISIPA	831
Qy	833	YVSTYGVKFSVAEVIALLASSFGLLGCIYFNKCVIILFKPCRNIEEVRGSTAAHAFKVA	892
Db	832	YVSTYGVKFSVAEVIALLASSFGLLGCIYFNKCVIILFKPCRNIEEVRGSTAAHAFKVA	891
Qy	893	ARATLRRSAAGRRSSSLCGSTISSPASSTCGPGLTMMQRCSTQKVSFGSGVTLSLSP	952
Db	892	ARATLRRSAAGRRSSSLCGSTISSPASSTCGPGLTMMQRCSTQKVSFGSGVTLSLSP	951
Qy	953	EETGRYATLSTARSNSADGRSGDILPSRHHDDGPPQKCEPOPANDARYKAAPTKGTLE	1012
Db	952	EETGRYATLSTARSNSADGRSGDILPSRHHDDGPPQKCEPOPANDARYKAAPTKGTLE	1011
Qy	1013	SPGGSKERPTTMEET	1027
Db	1012	SPGGSKERPTTMEET	1026
RESULT 7			
ID	AAU00508	standard; protein; 1059 AA.	
XX	AAU00508;		
XX	29-AUG-2001	(first entry)	
XX	Chicken	calcium-sensitive receptor (CaR) protein.	
KW	Avian; chicken;	calcium-sensing receptor; CaR; clone C1D;	
KW	extracellular	calcium homeostasis; parathyroid hormone; PTH;	
KW	serum	calcium regulator; bone deposition.	
XX	Gallus sp.		
Key	Location/Qualifiers		
Domain	1..611	/label= Extracellular domain	
FT	/note= "Amino-terminal predominantly hydrophilic domain"		
FT	1..19	/label= Signal_peptide	
FT	20..1059	/label= Mature_CaR_protein	
FT	136..165	/note= "Hydrophobic region characteristic of calcium-sensing receptors and metabotropic glutamate receptors"	
FT	612..861	/note= "Hydrophobic core comprising helical transmembrane domains"	
FT	862..1059	/note= "Carboxy-terminal hydrophilic domain"	
XX	US6210964-B1.		
XX	03-APR-2001.		
XX	14-AUG-1998;	98US-00134513.	
XX	19-AUG-1997;	97US-0058095P.	
XX	(BGHM )	BRIGHAM & WOMENS HOSPITAL INC.	
PI	Brown EM, Diaz R, Bai M, Quinn SJ;		
XX	WPI; 2001-289636/30.		
DR	N-PSDB; AAS01709.		
XX	New avian	calcium-sensing receptor polynucleotide and encoded receptor	
PT	protein, useful	for regulating serum concentration of calcium animals,	
PT	particularly	in chickens.	
XX	Claim 1; Fig 2A-2D;	43pp; English.	
XX			

CC	The present sequence representing an avian (chicken) calcium-sensing receptor (CaR) is isolated from chicken parathyroid gland cDNA clone CID.			
CC	CaR is involved in regulating extracellular calcium homeostasis by controlling PTH (parathyroid hormone) secretion. The polynucleotide encoding CaR is useful for producing calcium-sensing receptor protein, which can be used to regulate extracellular calcium homeostasis and to regulate serum calcium levels in chickens and related species. By increasing serum calcium, more rapid growth is obtained due to an increased rate of bone deposition, and eggs of higher quality are produced. A DNA construct comprising the CaR polynucleotide is useful for developing transgenic animals expressing a mutated form of the calcium-sensing receptor. The CaR polypeptide can be used to produce antibodies to CaR, which can be used to detect the presence of CaR protein using immunoassays. Also described are methods and compositions which can be used to modulate the serum concentration of calcium in humans and animals			
xx				
SQ	Sequence 1059 AA;			
QY	Query Match 75.9%; Score 4106.5; DB 4; Length 1059;			
DB	Best Local Similarity 76.4%; Pred. No. 0;			
QY	Matches 788; Conservative 85; Mismatches 130; Indels 29; Gaps 5;			
QY	1	MAQLHCQLLFLGFTLLQSNVSGYGNQRAQKGDIIILGGLPIHFGVAAKQODLKS RPE	60	
DB	1	MTLYSCCLILLFT---WNTAAYGNQRAQKGDIIILGGLPIHFGVAAKQODLKS RPE	56	
QY	61	ATKICIRNFRGFRWLQAMIFALBEINNSMTFLNITLGYRIPDTCNTVSKALEATLSFVA	120	
DB	57	SVEICIRNFRGFRWLQAMIFALBEINNSMTFLNITLGYRIPDTCNTVSKALEATLSFVA	116	
QY	121	QNKIDSINLDFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSN	180	
DB	117	QNKIDSINLDFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSYASSRLLSN	176	
QY	181	KNEYKAFRLTIPNDEQOATAMAEIIEHFQNWVGTAAADDDYGRGIDKFERBEAVKRDIC	240	
DB	177	KNOFKSFLRTIPNDEQOATAMAEIIEYFRNWVGTIAADDDYGRGIEKFERBEAERDIC	236	
QY	241	IDFSEMSIQYTKQLEFADVIQNSAKVIVVFSNGPDLEPLIQIVRENIIDRIWLAS	300	
DB	237	IDFSELSIQSDDEEIQOVVEIQNSTARVIVVFSNGPDLEPLIQIVRENIIDRIWLAS	296	
QY	301	EAWASSSLIAKPEYFHVVGCTIGFALRAGRIPOGPNFKLKEVHFSRSDNCGFVKEFWEETF	360	
DB	297	EAWASSSLIAKPEYFHVVGCTIGFALRAGRIPOGPNFKLKEVHFSRSDNCGFVKEFWEETF	356	
QY	361	NCYFTEKTLQLKNSKVPSPGPAQDGSKAGNSRRRTALRHPCTGENITSVETPYLDYT	420	
DB	357	NCYLPSES----KNSPASAFHKAHEGLGAGNG-TAAFPPTCTGENITSVETPYMDFT	411	
QY	421	HLRISYNNVAVYSIAHALQDIHSCKPGTGI FANGSCADIKKVEAWQVNLHLKPTNS	480	
DB	412	HLRISYNNVAVYSIAHALQDIHSCKPGTGI FANGSCADIKKVEAWQVNLHLKPTNS	471	
QY	481	MGEQVDFDDGDLKGNVTIINWOLSADESVLPHEVCNYYNAYAKPSDRNLNKKILWSG	540	
DB	472	MGEQVDFDFGLVGNYSIINWHLSPEDGVSFWVEVGHVNYAKKGERLFINENKILWSG	531	
QY	541	FSKVVPFNSGSRDCVPGTRKGIIEGEPTCCFECMACAEFSGDENASACTKCPNDFWSN	600	
DB	532	FSKEVPFNSGSRDCVPGTRKGIIEGEPTCCFECVDCPDGEVSDTASACDKCPEDWASN	591	
QY	601	ENHTSCIAKIEYLSWTEPFGIALTIIPAVILGILITSFVLGVFKFRNTPVKATNRELSY	660	
DB	592	ENHTSCIPKQIEFLSWTEPFGIALTLPAVLGIFLTSFVLGVFKFRNTPVKATNRELSY	651	
QY	661	LLASLLICCCSSSLIFIGEPDRDTCRLRQAPAGISFVLCISCLVKNRVLVPEAKIPT	720	
DB	652	LLLSLLICCCSSSLIFIGEPQNTCRLRQAPAGISFVLCISCLVKNRVLVPEAKIPT	711	
QY	721	SLHRKWWGLNQFLVFLCTFVQIVCVIWLTYAPPSSYRNHELEDEVIPTCEGSLMA	780	
DB	712	SLHRKWWGLNQFLVFLCTFVQIVCVIWLTYAPPSSYRNHELEDEVIPTCEGSLMA	771	

QY 781 LGFLIGVTCLLAAICFFFAKSKRLPENFNEAKFITFSMLIFFIVWISFIPAYSTYKGF 840  
Db 772 LGFLIGVTCLLAAICFFFAKSKRLPENFNEAKFITFSMLIFFIVWISFIPAYSTYKGF 831  
QY 841 VSAVEVAILASSGGLGCIYENKCYIIILFKCRNTIEVRCSHAHAFKVAARATLRS 900  
Db 832 VSAVEVAILAAGFGLLACIFENKCVIIILFKPSRNTIEVRCSHAHAFKVAARATLRS 891  
QY 901 AASRRSSSLGSGTSSPASSTCGPG-----LTMORCSTQKVSFGSGT 947  
Db 892 NVSRKRSNLGGSTGTPSSISSSKNHEDPPPLPASAERQQRQCKQKVSFGSGT 951  
QY 948 LSLSPETGRYATLSSTARSNSADGSDLLPSRHDDGPPKCEPQANDARYKAAPT 1007  
Db 952 LSLSPFEPQKNAMANNKRRNSLEAQNDSDDSLMRHALLAQ-----NSESLSABFG 1004  
QY 1008 KGTLESFGGSKE 1019  
Db 1005 FQTASSPETSSQ 1016  
RESULT 8  
ID AAU02195  
XX AAU02195 standard; protein; 1078 AA.  
AC AAU02195;  
XX  
DT 26-SEP-2001 (first entry)  
DE  
DE Cynomolgous monkey calcium-sensing receptor.  
KW Monkey; calcium-sensing receptor; bacteria; fungus; protozoa; viral;  
KW infection; HIV-1; HIV-2; human immunodeficiency virus; pain; cancer;  
KW diabetes; obesity; anorexia; bulimia; Parkinson's disease; stroke;  
KW acute heart failure; hypotension; hypertension; urinary retention;  
KW osteoporosis; angina pectoris; myocardial infarction; ulcer; asthma;  
KW allergy; benign prostatic hypertrophy; migraine; vomiting; psychotic;  
KW neurological disorder; anxiety; schizophrenia; manic depression;  
KW depression; delirium; dementia; severe mental retardation; dyskinesia;  
KW Huntington's disease; Gilles de la Tourette's syndrome; vaccine.  
XX  
OS Macaca cynomologus.  
XX  
PN WO200140252-A1.  
XX  
PD 07-JUN-2001.  
XX  
PF 01-DEC-2000; 2000WO-US032864.  
XX  
XX 01-DEC-1999; 99US-0168342P.  
PR 30-NOV-2000; 2000US-00727205.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
PI Ellis CE;  
XX  
DR WPI; 2001-408275/43.  
DR N-PSDB; AAS06331.  
XX  
XX Novel Cynomolgous Monkey Calcium-Sensing Receptor polypeptides are useful  
PT for treating infections, pain, cancer, diabetes, obesity, asthma,  
PT schizophrenia, hypertension, urinary retention, Parkinson's disease and  
PT stroke.  
XX  
XX Claim 2; page 28; 38pp; English.  
PS  
XX The sequence represents the amino acid sequence of Cynomolgous monkey  
CC calcium-sensing receptor. The calcium-sensing receptor nucleic acid and  
CC polypeptide are useful for treating bacterial, fungal, protozoan and  
CC viral infections, particularly infections caused by HIV-1 or HIV-2, pain,  
CC cancer, diabetes, obesity, anorexia, bulimia, Parkinson's disease, acute

CC heart failure, hypotension, hypertension, urinary retention,  
CC osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers,  
CC asthma, allergies, benign prostatic hypertrophy, migraine, vomiting,  
CC psychotic and neurological disorders including anxiety, schizophrenia,  
CC manic depression, depression, delirium, dementia and severe mental  
CC retardation, and dyskinesias, such as Huntington's disease or Gilles de  
CC la Tourette's syndrome. The polypeptide is useful for structure-based  
CC design of agonist, antagonist or inhibitor of the calcium-sensing  
CC receptor. The DNA sequence is useful for chromosome localisation studies.  
XX The polypeptide and nucleic acid are also useful as vaccines  
SQ Sequence 1078 AA;  
Query Match 75.0%; Score 4055.5; DB 4; Length 1078;  
Best Local Similarity 74.3%; Pred. No. 0;  
Matches 785; Conservative 85; Mismatches 136; Indels 51; Gaps 7;  
QY 1 MAQLHCOLLFLGFTLLQSYNVGYGNQRAQKGDIIILGGLFFIHFGVAAKODLKS RPE 60  
Db 1 MAFYCCFWLLALT-----WTSAYGDPQRAQKGDIIILGGLFFIHFGVAAKODLKS RPE 56  
QY 61 ATKIRYNFRGFWLQAMIFAIEEINNSMTFLPNITLGYRIFDTCTNTVSKALEATLSFVA 120  
Db 57 SVECIYNFRGFWLQAMIFAIEEINSSPALLPNLTGLYRIFDTCTNTVSKALEATLSFVA 116  
QY 121 QNKIDSINLDEFNCSDHIPSTIAVVGATGSGTAVANLLGLFYIPQVSYSSSLLSN 180  
Db 117 QNKIDSINLDEFNCSEHIPSTIAVVGATGSGTAVANLLGLFYIPQVSYSSSLLSN 176  
QY 181 KNEYKAFRTIPNDEQATAMAEIIEHFQNMVGTTLAADDYGRPGIDKFREEAVKRDIC 240  
Db 177 KNQFKSFLRTIPNDEHQATAMADIIEYFRNMVGTTLAADDYGRPGIEFREEAEERDIC 236  
QY 241 IDSEMSIYQYQKLEFADIVQNSAKVIVVFSNGPDLEPLIQEIVRNTIDRWLAS 300  
Db 237 IDSEMSIYQYDEEEIYHVVEIQNSAKVIVVFSNGPDLEPLIQEIVRNTIDRWLAS 296  
QY 301 EAWASSSLAKPYFHVVGTTGFALRAGRIQFNKFLXEVHPSSSDNGFVKEWEETFF 360  
Db 297 EAWASSSLAMPYFHVVGTTGFALRAGRIQFNKFLXEVHPSSSDNGFVKEWEETFF 356  
QY 361 NCVFTKTLTQLKNSKVPSSGPAAGDGSAGNSRRRTALRHPTGBENTTSVETPYDVT 420  
Db 357 NCHLQEGAKGPL---PVDTFLRHGHESSGGRFNS-STAFRPLCTGDNISSETPYDVT 412  
QY 421 HLRISYVAVYVYSIAHALQDIHSCKPGTGIFANGSCADIKKVAVQVLNHLHLKFTNS 480  
Db 413 HLRISYVAVYVYSIAHALQDIHSCKPGTGIFANGSCADIKKVAVQVLNHLHLKFTNS 472  
QY 481 MGEQVDFDQGLKNGYTTIINQLSAEDSVLFHEVGNYNAYAKPSDRLININEKILMSG 540  
Db 473 MGEQVDFDECGDLVGNYSIINWHLSPEDGSIYFKEVGYVYVYAKKGERLFINEEKILMSG 532  
QY 541 FSKVVPFNSCRDVPCTKGIIEGPCTCCFCMACAECEGFSDENDASACTCPDPSN 600  
Db 533 FSRVEVPFNSCRDCLAGTRKGIIEGPCTCCFCMACAECEGFSDENDASACTCPDPSN 592  
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLIGILITTSFVLGVFIKFRNTPIVKATNRELSY 660  
Db 593 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLIGILITTSFVLGVFIKFRNTPIVKATNRELSY 652  
QY 661 LLLFSLICFSSSLTIFIGEPDWTCLRLQPAIGISFVLCISILVKTNRVLLVFAKPT 720  
Db 653 LLLFSLICFSSSLTIFIGEPDWTCLRLQPAIGISFVLCISILVKTNRVLLVFAKPT 712  
QY 721 SLHRKRWGLNLOFLVFLCILVQIVTCIIWLVTAPPSSYRNHELEDEVIFITCDGSLMA 780  
Db 713 SPHRKRWGLNLOFLVFLCILVQIVTCIIWLVTAPPSSYRNHELEDEVIFITCDGSLMA 772  
QY 781 LGFLIGVTCLLAAICFFFAKSKRLPENFNEAKFITFSMLIFFIVWISFIPAYSTYKGF 840  
Db 773 LGFLIGVTCLLAAICFFFAKSKRLPENFNEAKFITFSMLIFFIVWISFIPAYSTYKGF 832





ID	AD62143 standard; protein; 1078 AA.	Db	1	MAFYSCWVLLALT---WHTSAYGPDQRAQKGDIIILGGLPFIHFGVAAKDDLSRPE	56
XX	AD62143;	Qy	61	ATKIRYNFRGFRWLQAMIFAIEEINNMTFPIITLGYRIFDTCTNTVSKALEATLSFVA	120
XX		Db	57	SVECIYNFRGFRWLQAMIFAIEEINSPALLPNTLGYRIPTDCTNTVSKALEATLSFVA	116
DT	29-JAN-2004 (first entry)	Qy	121	ONKIDSLNDEFNCSDHIPSTIATVVGATGSGISTAVANLLGLFYIPOVSYASSSSLLSN	180
XX	Human Protein P41180, SEQ ID NO 8072.	Db	117	QNKIDSLNDEFNCSEHIPSTIATVVGATGSGISTAVANLLGLFYIPOVSYASSSSLLSN	176
XX	Human; pain; neuronal tissue; gene therapy;	Qy	181	KNYKAPLRTIPNDEQATAMAEIIEHFWNMVGTIAADDDYGRPGIDKFRBAAVRDIC	240
KW	spinal segmental nerve injury; chronic constriction injury; CCI;	Db	177	KNQFKSFLRTIPNDEHQATAMADIIIFRNWVGTIAADDDYGRPGIEKFRBAAVRDIC	236
KW	spared nerve injury; SNI; Chung.	Qy	241	IDFSEMITQYTKOLEFIADVIQNSAKVIVVFSNGPDLEPLIQIBIVRNITDRIWLAS	300
OS	Homo sapiens.	Db	237	IDFSELSIQSYDEEIQHVVEVIQNSTAKVIVVFSNGPDLEPLIKIIVRNITGKIWLAS	296
XX	WO2003016475-A2.	Qy	301	EAWASSLIAKPEYFHVVGTTGTFALRAGRIPOFNKFLKEVHPSRSDNGFVKERWEET	360
XX	27-FEB-2003.	Db	297	EAWASSLIAKPEYFHVVGTTGTFALRAGRIPOFNKFLKEVHPSRSDNGFVKERWEET	356
XX	14-AUG-2002; 2002WO-US025765.	Qy	361	NCVTEKTLTQKNSKVPVSHGPAAGDGSKAGNSRRTALRHPCTGEENITSVETPYDYT	420
XX	14-AUG-2001; 2001US-0312147P.	Db	357	NCHLEGAKGPL---PVDIFLRGHEBSGDRFNS-STARPLCTGDENISSVETPYDYT	412
PR	01-NOV-2001; 2001US-0346382P.	Qy	421	HLRISYVYVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAQVNLHLHLKFTNS	480
PR	26-NOV-2001; 2001US-0333347P.	Db	413	HLRISYVYVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAQVNLHLHLKFTNN	472
XX	(GENO ) GEN HOSPITAL CORP.	Qy	481	MGEQVDFDQDGLKGNVTIINWOLSAEDSVLFEVGNVAYAKPSDRNLNKKILWSG	540
PA	(FARB ) BAYER AG.	Db	473	MGEQVDFDQDGLKGNVTIINWOLSAEDSVLFEVGNVAYAKPSDRNLNKKILWSG	532
XX	Woolf C, D'urso D, Befort K, Costigan M;	Qy	541	FSKVPFNSCSDCVPTGRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPNDFWSN	600
DR	WPI: 2003-268312/26.	Db	533	FSREVPFNSCSDCVPTGRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPNDFWSN	592
XX	GENBANK; P41180.	Qy	601	ENHTSCIAKIEVLSWTEPEGIALTFVNLGILITSVLGVFKFTKNTPIVKATNRELSY	660
XX	New composition comprising two or more isolated polypeptides, useful for	Db	593	ENHTSCIAKIEVLSWTEPEGIALTFVNLGILITSVLGVFKFTKNTPIVKATNRELSY	652
PT	preparing a medicament for treating pain in an animal.	Qy	661	LLFSLTCCFSSSILFGEPRDWTCLRQAPAFGISFVLCISILVKNRVLLVFEAKIPT	720
PS	Claim 1; Page; 1017pp; English.	Db	653	LLFSLTCCFSSSILFGEPRDWTCLRQAPAFGISFVLCISILVKNRVLLVFEAKIPT	712
CC	The invention discloses a composition comprising two or more isolated rat	Qy	721	SLHRKWLNLQFLVLCILVOITCIWLYTAPSSYRNHELEDEVIFITCEGSLMA	780
CC	or human polynucleotides or a polynucleotide which represents a fragment,	Db	713	SFHRKWLNLQFLVLCILVOITCIWLYTAPSSYRNHELEDEVIFITCEGSLMA	772
CC	derivative or allelic variation of the nucleic acid sequence. Also	Qy	781	LGFLIGVTCLLAICFFFAFKSKLPENFNEAKFITFMSLIFFIWISPIPAYVSTYVKF	840
CC	claimed are a vector comprising the novel polynucleotide, a host cell	Db	773	LGFLIGVTCLLAICFFFAFKSKLPENFNEAKFITFMSLIFFIWISPIPAYVSTYVKF	832
CC	comprising the vector, a method for identifying a nucleotide sequence	Qy	841	VSAVEVIAILASSFGLLGCTYFNKCVIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS	900
CC	which is differentially regulated in an animal subjected to pain and a	Db	833	VSAVEVIAILASSFGLLGCTYFNKCVIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS	892
CC	kit to perform the method, an array, a method for identifying an agent	Qy	901	AASRKSSTLGGSTISSPASSTCGPG-----LTMEM	931
CC	that increases or decreases the expression of the polynucleotide sequence	Db	893	NVRKSSSSLGSGTSGTSSSSISKNSNEDPFPQPERKQOQOQPLATQOQOQOQPLTPQ	952
CC	that is differentially expressed in neuronal tissue of a first animal	Qy	932	Q-----RCSTOKVFSGSGTSLTSLSFETGYATLSRTARSNRNADGRSGDPLFSRHH	984
CC	subjected to pain, a method for identifying a compound which regulates	Db	953	QORSQOQPRCK-QKVIIFSCTVTFSLSFDEPQKNAMAHNRNTHQNSLEAQKSSDTLTRH-	1010
CC	the expression of a polynucleotide sequence which is differentially	Qy	985	DQGPPOKCEPQANDARYKAAPTGTILSPGGSKERP	1021
CC	expressed in an animal subjected to pain, a method for identifying a	Db	1011	-----QPLFLQCGTDLDTLTVQETGLQGPVGGDQRP	1042
CC	compound that regulates the activity of one or more of the	Qy			
CC	polynucleotides, a method for producing a pharmaceutical composition, a	Db			
CC	method for identifying a compound or small molecule that regulates the	Qy			
CC	activity in an animal of one or more of the polypeptides given in the	Db			
CC	specification, a method for identifying a compound useful in treating	Qy			
CC	pain and a pharmaceutical composition comprising the one or more	Db			
CC	polypeptides or their antibodies. The polynucleotide or the compound that	Qy			
CC	modulates its activity is useful for preparing a medicament for treating	Db			
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction	Qy			
CC	injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene	Db			
CC	therapy). The sequence presented is a human protein (shown in Table 2 of	Qy			
CC	the specification) which is differentially expressed during pain. Note:	Db			
CC	The sequence data for this patent did not form part of the printed	Qy			
CC	specification, but was obtained in electronic form directly from WIPO at	Db			
CC	ftp.wipo.int/pub/published_pct_sequences.	Qy			
XX	Sequence 1078 AA;	Db			
SQ	Query Match 74.8%; Score 4044.5; DB 7; Length 1078;	Qy			
	Best Local Similarity 74.0%; Pred. No. 0;	Db			
	Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;	Qy			
	1 MAQLHCQLLFLGFTLLQSNVSGVGNQRAQKGDIIILGGLPFIHFGVAAKDDLSRPE 60	Db			

RESULT 12  
ADE62147





ID	ADH10955 standard; protein; 1078 AA.	
XX	ADH10955;	
AC	ADH10955;	
XX	11-MAR-2004 (first entry)	
DT	Human parathyroid calcium receptor (HuPcar) protein.	
XX	polyvalent cation sensing receptor; pVCR; Atlantic salmon;	
DE	growth increase; mortality reduction; human;	
KW	parathyroid calcium receptor; HuPcar.	
XX	Homo sapiens.	
XX	WO2003087331-A2.	
PN	23-OCT-2003.	
PD	09-APR-2003; 2003WO-US011188.	
XX	11-APR-2002; 2002US-00121441.	
PF	18-APR-2002; 2002US-00125772.	
XX	18-APR-2002; 2002US-00125778.	
PR	18-APR-2002; 2002US-00125792.	
XX	(MARI-) MARICAL INC.	
PA	Harris HW, Nearing J, Betka M;	
XX	WPI; 2003-845319/78.	
XX	New Atlantic salmon polyvalent cation-sensing receptor, pVCR,	
PT	polyptides useful in commercial raising of salmon and restoration of	
PT	wild Atlantic salmon populations especially in transfer from freshwater	
PT	to seawater.	
XX	Disclosure; SEQ ID NO 30; 269pp; English.	
PS	The invention comprises the amino acid and coding sequences of polyvalent	
XX	cation sensing receptor (pVCR) proteins from Atlantic salmon. The DNA and	
CC	protein sequences of the invention are useful in the commercial raising	
CC	of Atlantic salmon and the restoration of wild Atlantic salmon	
CC	populations, especially in the transfer from freshwater to seawater with	
CC	increased growth and reduced mortality. The present amino acid sequence	
CC	represents the human parathyroid calcium receptor (HuPcar) protein.	
XX	Sequence 1078 AA;	
SQ	Query Match 74.8%; Score 4044.5; DB 7; Length 1078;	
	Best Local Similarity 74.0%; Pred. No. 0; Mismatches 138; Indels 51; Gaps 7;	
	Matches 782; Conservative 86;	
QY	1 MAQLHCQLLFLGFTLLQSYNVSQGNORAKKGDIIILGGLPPIHFGVAAKDQDLKSRPE 60	
Db	1 MAFYSQVLLALT---WHTSAYGPDQRAQKKGDIILGGLPPIHFGVAAKDQDLKSRPE 56	
QY	61 ATKCYRNPGRFRWLOAMIFAEERINNSMTFLPNTLGYRIPDTCNTVSKALEATLSVA 120	
Db	57 SVECYRNPGRFRWLOAMIFAEERINNSMTFLPNTLGYRIPDTCNTVSKALEATLSVA 116	
QY	121 QNKIDSLNDEFNCNSDHPIPTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSN 180	
Db	117 QNKIDSLNDEFNCNSDHPIPTIAVVGATGSGISTAVANLLGLFYIPQVSYASSSRLLSN 176	
QY	181 KNEYKAFRTTIPNDQQATAMAEIIEHFQWNNWGTAAADDDYGRGIDKIFREEAVKRDIC 240	
Db	177 KNQKSFRTIIPNDQQATAMAEIIEHFQWNNWGTAAADDDYGRGIDKIFREEAVKRDIC 236	
QY	241 IDFSEMSIOYVTKOLEFTADYVIONSSAKVIIVFSGNDPDLPLDIEIVRNITDRIWLAS 300	
Db	237 IDFSELSIQSDEEEIQHVVEVIQNSTAKVIIVFSGNDPDLPLDIEIVRNITDRIWLAS 296	
QY	301 EAWSSSLTAKPEYFHVVGTTIGFALRAGRIFGNKFLKEVHPSRSSDNGFVKFEWETTF 360	

Db	297 EAWSSSLTAMPQYFHVVGTTIGFALRAGRIFGNKFLKEVHPSRSSDNGFVKFEWETTF 356	
QY	361 NCYFTEKTLTQKNSKVPSPHGAQDGSKAGNSRRRTALRHPCGTBENITSVETPLDYT 420	
Db	357 NCHLQEGAGKPL---PVDTFLRGHEESGDRFNS-STAPRLCTGDNISSETPIDIT 412	
QY	421 HLRISYNYVAVYSIAHALQDIHSCXPGTGIFANGSCADIKKVEAMQVNLHLHLKFTNS 480	
Db	413 HLRISYNYVAVYSIAHALQDIHSCXPGTGIFANGSCADIKKVEAMQVNLHLHLFTNN 472	
QY	481 MGEQVDFDQDGLKGNYYIINWLSAEDSVLFHEVGNVNAVAKPSDRNLNINEKILNSG 540	
Db	473 MGEQVTFDECGDLVGNYSIINWLSAEDSVLFHEVGNVNAVAKPSDRNLNINEKILNSG 532	
QY	541 FSKVVPFNSCRDVPGRKGIIEGPTCCFECMACAEGEFGSDENDASACTKCPDNFWSN 600	
Db	533 FSEVPFNSCRDCLAGTRKGIIEGPTCCFECVCEPDEYDETDASACNCPDFFWSN 592	
QY	601 ENHTSCIAKEIEYLSWTEPFGIATITFAVLGILITSFVLGVIFKFRNTPIVATNRELSY 660	
Db	593 ENHTSCIAKEIEYLSWTEPFGIATITFAVLGILITSFVLGVIFKFRNTPIVATNRELSY 652	
QY	661 LLLFSLICCFSSSLIFIGPRDWTCLROPAGISFVLCISCLVKTNEVLLVFEAKIPT 720	
Db	653 LLLFSLICCFSSSLIFIGPRDWTCLROPAGISFVLCISCLVKTNEVLLVFEAKIPT 712	
QY	721 SLHRKWGLNLQFLVFLCLIVQITCIILWLTAPSSYRNHELEDEVIFITCDEGSLMA 780	
Db	713 SFHRKWGLNLQFLVFLCLIVQITCIILWLTAPSSYRNHELEDEVIFITCDEGSLMA 772	
QY	781 LGFLIGYTCLLAAICFFFAFKSKLPENNEAKFITFSMLIFPIVWISIPAVSVYKGF 840	
Db	773 LGFLIGYTCLLAAICFFFAFKSKLPENNEAKFITFSMLIFPIVWISIPAVSVYKGF 832	
QY	841 VSAVEVIAILASSFGLLGCIYFNKCIILFKPCRNITIEEVRCSTAAHAFKVAARATLRS 900	
Db	833 VSAVEVIAILASSFGLLGCIYFNKCIILFKPCRNITIEEVRCSTAAHAFKVAARATLRS 892	
QY	901 AASRKSSSLCGSTISSPASSTCGPG-----LTMEM 931	
Db	893 NVSRKSSSLCGSTISSPASSTCGPG-----LTMEM 952	
QY	932 Q-----RCSTOKVSGSGTWTLSLFEETGYATLSRTARSNSADGRSGDDPLSRHH 984	
Db	953 QRSQQPRCK-QRVIFGSGTWTLSLFEETGYATLSRTARSNSADGRSGDDPLSRHH 1010	
QY	985 DQPPPKCEPQANDARYKAAPTCKGTLESFGSGSKERP 1021	
Db	1011 -----QPLLLPQCGETDLDLTVQETGLQGVGDQRP 1042	
RESULT 14	ADJ68365	
ID	ADJ68365 standard; protein; 1078 AA.	
XX	ADJ68365;	
AC	ADJ68365;	
XX	06-MAY-2004 (first entry)	
DT	Human heat mitochondrial protein as a therapeutic target SeqID171.	
XX	Mitochondrial; human; screening assay; diabetes mellitus;	
XX	Huntington's disease; osteoarthritis;	
KW	Leber's hereditary optic neuropathy; LHON;	
KW	Mitochondrial encephalopathy lactic acidosis and stroke; MELAS;	
KW	myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;	
KW	neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;	
KW	osteopathic; ophthalmological; cytostatic.	
OS	Homo sapiens.	
XX	WO2003087768-A2.	

XX PD 23-OCT-2003.

XX PF 04-APR-2003; 2003WO-US010870.

XX PR 12-APR-2002; 2002US-0372843P.

XX PR 17-JUN-2002; 2002US-0389987P.

XX PR 20-SEP-2002; 2002US-0412418P.

XX PA (MITO-) MITOKOR.

XX PA (BUCK-) BUCK INST AGE RES.

XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;

XX PI Warnock DE;

XX DR WPI; 2003-845369/78.

XX PT Identifying a mitochondrial target for drug screening assays and for

XX PT treating diseases associated with altered mitochondrial function,

XX PT comprises detecting a modified polypeptide in a sample and correlating

XX PT with the disease.

XX PS Claim 1; SEQ ID NO 171; 180pp; English.

XX CC This invention relates to novel mitochondrial targets that can be used

XX CC for therapeutic intervention in treating a disease associated with

XX CC altered mitochondrial function. Specifically, it refers to a method for

XX CC identifying proteins of the human heart mitochondrial proteome that are

XX CC useful for drug screening assays, as well as therapeutic targets. The

XX CC present invention describes a method for identifying such proteins that

XX CC can be used in the treatment of various diseases associated with altered

XX CC mitochondrial function including diabetes mellitus, Huntington's disease,

XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial

XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy

XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these

XX CC compositions have neuroprotective, neurotropic, antidiabetic, and

XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological, and

XX CC cytoskeletal activities. This polypeptide sequence is a human heart

XX CC mitochondrial protein of the invention.

XX SQ Sequence 1078 AA;

Query Match 74.8%; Score 4044.5; DB 7; Length 1078;

Best Local Similarity 74.0%; Pred. No. 0; Mismatches 138; Indels 51; Gaps 7;

Matches 782; Conservative 86;

1 MAQLHCQLLFLGFTLLQSNVSGYGNQRAQKGGDILGGLFPIHFGVAARDQDLKSRPE 60

1 MAFYSCWVLLALT---WHTSAYGPDQRAQKGGDILGGLFPIHFGVAARDQDLKSRPE 56

61 ATKCRYNFRGRWLOAMFAIEEINNSMTFLPNTLGYRIEDTCTNTYSKALEATLSFVA 120

57 SVECRYNFRGRWLOAMFAIEEINNSPALPNTLGYRIEDTCTNTYSKALEATLSFVA 116

121 QNKIDSLNDFECNSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180

117 QNKIDSLNDFECNSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 176

181 KNEYXAFRTINDQQATANAIEIHFQWNVGTAAADDYGRPIDKFAEAVGRDIC 240

177 KNQKSFRTINDEHQATADADIEYFRWNVGTAAADDYGRPIDKFAEAVGRDIC 236

241 IPFSMISQYTKOLEFTADYQNSAKVIVFSGNDPLRLQEIIVRNITDRIMLAS 300

237 IPFSELISQYDEEIRHQVVEVQNSTAKVIVFSGNDPLRLQEIIVRNITDRIMLAS 296

301 EAWASSLSIAKPEYFHVVGTTGFPALRAGRIPGKNFLKEVHPGRSSDNGFKFWEETF 360

297 EAWASSLSIAKPEYFHVVGTTGFPALRAGRIPGKNFLKEVHPGRSSDNGFKFWEETF 356

361 NCYFTEKTLTQKNSKVPSHGPAAGDQSKAGNSRTALRHPCTGEENITSVETPYLDYT 420

357 NCHLQEGAKGPL---PVDFTLRGHESGDRFNS--STAFLPLCTGDENISSVETPYLDYT 412

QY 421 HLRISNVYVAVYSIAHALODIHSCKPGTGI FANGSCADIKKVEAMQVNLHLHLKFTNS 480

DB 413 HLRISNVYVAVYSIAHALODIYITCLPGRGLFNGSCADIKKVEAMQVNLHLHLNFTNN 472

QY 481 MGEQVDFDDQDLKNGYTIINWQLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILWSG 540

DB 473 MGEQVTFDECGDLVGNYSIINWHLSPEDGSI VFEKGVYNNVYAKGERLFINBEKILWSG 532

QY 541 FSKVVPESNCRDPCVGTGRKGIIEGPTCCFECMACAGEFSDENASACTKCPNDPWSN 600

DB 533 FSEVPESNCRDCLAGTRKGIIEGPTCCFECVCEPDGEYSDETASACNCKCPDFFWSN 592

QY 601 ENHTSCIATKIEIYLSWTEPFGIALTIFAVLIGLITITFVLGVFKFRNTPIVKATNRELSY 660

DB 593 ENHTSCIATKIEIYLSWTEPFGIALTIFAVLIGLITITFVLGVFKFRNTPIVKATNRELSY 652

QY 661 LLLFSLICCFSSSLIFIGEPDRWTCRLRQAPAGISFVLICISILVKNRVLVFEAKIPT 720

DB 653 LLLFSLICCFSSSLUFFIGEPQDWTCRLRQAPAGISFVLICISILVKNRVLVFEAKIPT 712

QY 721 SLHRKVGMLNQLVFLVLCILVOITCIWLVTAPPSSYRNHELEDEVIFITCDEGLMA 780

DB 713 SFRKRWGMLNQLVFLVLCITFMOIVICVWLVTAPPSSYRNQLEDEIIFITCHEGLMA 772

QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFIVWISFIPAVSYGKF 840

DB 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFIVWISFIPAVSYGKF 832

QY 841 VSAVEVTAIASSFGLLGCIYFNKCVIILFKPCNTIEVRCSTAAHAFKVAARATLRS 900

DB 833 VSAVEVTAIASSFGLLGCIYFNKCVIILFKPCNTIEVRCSTAAHAFKVAARATLRS 892

QY 901 AASRKSSSLCGSTISSPASSTCGPG-----LTMEM 931

DB 893 NVSRKSSSLGGSTGTSTPSSISSKNSSEDPPOPERKQOQPLALTQEQEQOQPLTLPO 952

QY 932 Q-----RCSTOKVSGGTVTLSLSPETGRYATLSRTARSNSADGRSGDDLPSSRH 984

DB 953 QRSQOQPRCK-QKVIFGSGTFTLSLSPDEQKNVAHRNSTHONSLEAKQSGDSTLTRH- 1010

QY 985 DQGPPOKCEPOPANDARYKAAPTKGTLESFGGSKERP 1021

DB 1011 -----QPLLPLOCGETDLDLTWQETGLQGVGDQRP 1042

RESULT 15

ADI41014

ID ADI41014 standard; protein; 1078 AA.

XX AC ADI41014;

XX DT 22-APR-2004 (first entry)

XX DE Human GPCR CASR #2.

XX KW Receptor; GPCR; G protein-coupled receptor; reproductive disorder;

XX KW testicular disorder; vas deferens disorder; spermatogenesis; infertility;

XX KW XX male; epididymitis; cryptorchidism; sperm transport disorder;

XX KW testicular cancer; testicular germ cell tumour; male hormone disorder;

XX KW premature puberty; Kallman syndrome; Cushing's syndrome; immune disorder;

XX KW leukaemia; arthritis; asthma; AIDS; rheumatoid arthritis;

XX KW inflammatory bowel disease; sepsis; T-cell mediated cytotoxicity;

XX KW graft-versus-host disease; autoimmunity disorder;

XX KW systemic lupus erythematosus; drug induced haemolytic anaemia;

XX KW Sjogren's disease; T-cell maturation disorder;

XX KW B-cell maturation disorder; vascular disorder; stroke; ischaemia;

XX KW myocardial infarction; atherosclerosis; gastrointestinal disorder; ulcer;

XX KW pulmonary disorder; brain disorder; endocrine disorder; cancer;

XX gene therapy.

XX OS Homo sapiens.

XX XX

PN	US2004018976-A1.	Best Local Similarity 74.0%; Pred. No. 0;			
XX	29-JAN-2004.	Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;			
XX	13-MAY-2003; 2003US-00436715.				
XX	14-MAY-2002; 2002US-0380336P.				
XX	(FEDE/) FEDER J N.				
PA	(MINT/) MINTIER G.				
PA	(RAMA/) RAMANATHAN C S.				
XX	Feder JN, Mintier G, Ramanathan CS;				
XX	WPI; 2004-122081/12.				
XX	New human G-protein coupled receptor polypeptide and polynucleotide,				
PT	useful for diagnosing, preventing, treating or ameliorating a medical				
PT	condition, e.g. reproductive disorder, immunodeficiency disease or				
PT	testicular cancer.				
XX	Disclosure; SEQ ID NO 74; 290pp; English.				
XX	The invention relates to an isolated human G protein-coupled receptor				
CC	polypeptide and its encoding polynucleotide, including the full length				
CC	proteins minus the start methionine (and the region of the polynucleotide				
CC	encoding this protein region). The proteins are designated HGPBMX30-1,				
CC	HGPBMX30-2, HGPBMX30-3, HGPBMX41-1, HGPBMX41-2, HGPBMX41-3, and				
CC	HGPBMX42, HGPBMX42-1, HGPBMX43 and HGPBMX44. Also included are				
CC	expression vectors, host cells, antibodies, preventing (treating or				
CC	ameliorating) a medical condition comprising administering to a mammalian				
CC	subject the polypeptide or its modulator and diagnosing a pathological				
CC	condition or a susceptibility to a pathological condition in a subject				
CC	(comprising determining the presence or absence of a mutation in the				
CC	polynucleotide, or the presence or amount of expression of the				
CC	polypeptide in a biological sample and diagnosing a pathological				
CC	condition or a susceptibility to a pathological condition based on the				
CC	presence or absence of the mutation, or the presence or amount of				
CC	expression of the polypeptide). The human G-protein coupled receptor				
CC	polypeptide or polynucleotide can be used for diagnosing a pathological				
CC	condition or a susceptibility to a pathological condition in a subject,				
CC	and for preventing, treating or ameliorating a medical condition, such as				
CC	a disorder related to aberrant G-protein coupled receptor activity, a				
CC	disorder related to aberrant signal transduction, a reproductive disorder				
CC	; a male reproductive disorder, a testicular disorder, a vas deferens				
CC	disorder, spermatogenesis, infertility, Klinefelter's syndrome, XX male,				
CC	epididymitis, genital warts, germinal cell aplasia, cryptorchidism,				
CC	varicocele, immobile cilia syndrome, viral orchitis, sperm transport				
CC	disorders, testicular cancer, choriocarcinoma, non-seminoma, seminoma,				
CC	testicular germ cell tumors, male hormone disorders, premature puberty,				
CC	incomplete puberty, Kallman syndrome, Cushing's syndrome, an immune				
CC	disorder, a proliferative immune disorder, leukaemia, arthritis, asthma,				
CC	immunodeficiency diseases such as AIDS, rheumatoid arthritis,				
CC	granulomatous disease, inflammatory bowel disease, sepsis, acne,				
CC	neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell				
CC	mediated cytotoxicity, immune reactions to transplanted organs and				
CC	tissues, such as host-versus-graft and graft-versus-host diseases, or				
CC	autoimmunity disorders, such as autoimmune infertility, demyelination,				
CC	systemic lupus erythematosus, drug induced haemolytic anaemia, Sjogren's				
CC	disease, scleroderma, T-cell maturation disorders, B-cell maturation				
CC	disorders, vascular disorders, stroke, ischaemia, myocardial infarction,				
CC	atherosclerosis, embolisms, thrombosis, gastrointestinal disorders,				
CC	irritable bowel syndrome, ulcers, pulmonary disorders, brain disorders,				
CC	endocrine disorders, or ovarian, stomach, colon or kidney cancer or its				
CC	related proliferative condition (many other diseases and disorders are				
CC	listed in the specification). The antibodies may be used to purify,				
CC	detect and target the G-protein coupled receptor polypeptides. The				
CC	polynucleotides are also useful in gene therapy. The present sequence				
CC	represents a species homologue of a novel GPCR of the invention.				
XX	Sequence 1078 AA;				
XX	Query Match 74.6%; Score 4044.5; DB 8; Length 1078;				

Thu Nov 18 06:53:34 2004

us-10-016-496-2.rag

Page 16

Db 1011 -----QPLLPLOGETDLDLTVQETGLQGPVGGDQRP 1042

Search completed: November 17, 2004, 11:50:12  
Job time : 308 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2004, 11:06:04 ; Search time 125 Seconds  
(without alignments)  
544.869 Million cell updates/sec

Title: US-10-016-496-2  
Perfect score: 5410  
Sequence: 1 MAQHCOLLFLGFTLLQSYN.....KGTLESPGGSKERTTVEET 1027

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5410	100.0	1027	3	US-09-162-021B-2
2	5410	100.0	1027	4	US-10-268-051-8
3	4106.5	75.9	1059	3	US-09-134-513-2
4	4037.5	74.6	1078	1	US-08-485-588-7
5	4037.5	74.6	1078	1	US-08-484-565-7
6	4037.5	74.6	1078	2	US-08-480-751-7
7	4037.5	74.6	1078	2	US-08-943-986-7
8	4037.5	74.6	1078	3	US-08-353-784-7
9	4037.5	74.6	1078	3	US-08-484-719B-7
10	4037.5	74.6	1078	3	US-08-484-159-7
11	4029.5	74.5	1088	1	US-08-485-588-6
12	4029.5	74.5	1088	1	US-08-484-565-6
13	4029.5	74.5	1088	2	US-08-480-751-6
14	4029.5	74.5	1088	2	US-08-943-986-6
15	4029.5	74.5	1088	3	US-08-353-784-6
16	4029.5	74.5	1088	3	US-08-484-719B-6
17	4029.5	74.5	1088	3	US-08-484-159-6
18	3999.5	73.9	1085	1	US-08-485-588-5
19	3999.5	73.9	1085	1	US-08-484-565-5
20	3999.5	73.9	1085	2	US-08-480-751-5
21	3999.5	73.9	1085	2	US-08-943-986-5
22	3999.5	73.9	1085	3	US-08-353-784-5
23	3999.5	73.9	1085	3	US-08-484-719B-5
24	3999.5	73.9	1085	3	US-08-484-159-5
25	3996	73.9	1079	1	US-08-485-588-8
26	3996	73.9	1079	1	US-08-484-565-8
27	3996	73.9	1079	2	US-08-480-751-8

Sequence 8, Appli  
Sequence 8, Appli  
Sequence 8, Appli  
Sequence 8, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 5, Appli  
Sequence 5, Appli  
Sequence 8, Appli  
Sequence 10, Appli  
Sequence 12, Appli  
Sequence 12, Appli  
Sequence 12, Appli  
Sequence 14, Appli  
Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-162-021B-2

; Sequence 2, Application US/09162021B

; Patent No. 6337391

; GENERAL INFORMATION:

; APPLICANT: H. William Harris

; APPLICANT: Edward M. Brown

; APPLICANT: Steven C. Hebert

; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic

; TITLE OF INVENTION: Species and Methods of Use Thereof

; FILE REFERENCE: 2856.1001-007

; CURRENT APPLICATION NUMBER: US/09/162,021B

; CURRENT FILING DATE: 1998-09-28

; PRIOR APPLICATION NUMBER: PCT/US97/05031

; PRIOR FILING DATE: 1997-03-27

; PRIOR APPLICATION NUMBER: 08/622,738

; PRIOR FILING DATE: 1996-03-27

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 1027

; TYPE: PRT

; ORGANISM: squalus acanthias

US-09-162-021B-2

Query Match 100.0%; Score 5410; DB 3; Length 1027;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAQHCOLLFLGFTLLQSYNVSQYGNQRAQKGDIIILGGLFFIHFGVAAKDQDLKS RPE 60

Db 1 MAQHCOLLFLGFTLLQSYNVSQYGNQRAQKGDIIILGGLFFIHFGVAAKDQDLKS RPE 60

Qy 61 ATKCI RY NFRGFRWLQAMTFAIEEINNSMTFLPNITLGVRIPTCTNTVSKALEATLSFVA 120

Db 61 ATKCI RY NFRGFRWLQAMTFAIEEINNSMTFLPNITLGVRIPTCTNTVSKALEATLSFVA 120

Qy 121 QNKIDS LNLDFE NCSDHPISTIAVVGATGSGSTAVANLLGLFYIPQVSYASSSRLLSN 180

Db 121 QNKIDS LNLDFE NCSDHPISTIAVVGATGSGSTAVANLLGLFYIPQVSYASSSRLLSN 180

Qy 181 KNEYKAF LRTIPNDEQQATAMAEIIIEHFQWNWVGTLLAADDDYGRPGIDKFRFEAVKRDIC 240

Db 181 KNEYKAF LRTIPNDEQQATAMAEIIIEHFQWNWVGTLLAADDDYGRPGIDKFRFEAVKRDIC 240

Qy 241 IDPSEMI SQYTKQLFEIADVTQNSSAKVIVVPSNGPDLEPLIOEIVRNITDRWLAS 300

Db 241 IDPSEMI SQYTKQLFEIADVTQNSSAKVIVVPSNGPDLEPLIOEIVRNITDRWLAS 300

Qy 301 EAWSSSLIAKPEYFHVVGTTIGTFALRAGRIPGNKFLKEVHPSRSSDNGFVKEFWEETF 360

Db 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRI PGFNKFLKEVHPSSRSDNGFVKFEWEEFT 360  
QY 361 NCYFTEKTLTQKNSKVPBGHGAAGDQSGKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420  
Db 361 NCYFTEKTLTQKNSKVPBGHGAAGDQSGKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420  
QY 421 HLRISVNVVAVYSIAHALQDIHSCKPGTGI FANGSCADIKKVEAWQVNLHLHLKFTNS 480  
Db 421 HLRISVNVVAVYSIAHALQDIHSCKPGTGI FANGSCADIKKVEAWQVNLHLHLKFTNS 480  
QY 481 MGEQVDFDQGDILKGNYYTIINWQSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILMSG 540  
Db 481 MGEQVDFDQGDILKGNYYTIINWQSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILMSG 540  
QY 541 FSKVVPFNSCRDCVPGTRKGIIEGPTCCFECMACAEGEFDENDASACTKCPNDFWSN 600  
Db 541 FSKVVPFNSCRDCVPGTRKGIIEGPTCCFECMACAEGEFDENDASACTKCPNDFWSN 600  
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY 660  
Db 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY 660  
QY 661 LLLFSLICCFSSSLIFIGEPDRWTCRLRQPAFGISFVLCISILVKTNRVLLVFEAKIPT 720  
Db 661 LLLFSLICCFSSSLIFIGEPDRWTCRLRQPAFGISFVLCISILVKTNRVLLVFEAKIPT 720  
QY 721 SLHRKWVGNLQFLVFLCILVQITVCIIWLTAPPSYRNHELEDEVIFITCDGSLMA 780  
Db 721 SLHRKWVGNLQFLVFLCILVQITVCIIWLTAPPSYRNHELEDEVIFITCDGSLMA 780  
QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFEAKFTFSNLFFIWMISFIPAYVSTYKGF 840  
Db 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFEAKFTFSNLFFIWMISFIPAYVSTYKGF 840  
QY 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900  
Db 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900  
QY 901 AASRKSSSLCGSTISSPASSTCGGLTMEMORCSTQKVSFGSGVTLSLFEETGRYAT 960  
Db 901 AASRKSSSLCGSTISSPASSTCGGLTMEMORCSTQKVSFGSGVTLSLFEETGRYAT 960  
QY 961 LGRTARSNSADGRSGDDLPSRHDPQGPQKCEPOPANDARYKAAPTGTLESFGGSKER 1020  
Db 961 LGRTARSNSADGRSGDDLPSRHDPQGPQKCEPOPANDARYKAAPTGTLESFGGSKER 1020  
QY 1021 PTMTEET 1027  
Db 1021 PTMTEET 1027

## RESULT 2

US-10-268-051-8  
; Sequence 8, Application US/10268051  
; Patent No. 6748900  
; GENERAL INFORMATION:  
; APPLICANT: Harris, H. William  
; APPLICANT: Jurry, Steven  
; APPLICANT: Russell, David R.  
; APPLICANT: Neuring, Jacqueline A  
; APPLICANT: Betka, Marlies  
; APPLICANT: Linley, Timothy  
; APPLICANT: Brown, Edward M  
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant  
; FILE REFERENCE: 2213.2004-001  
; CURRENT APPLICATION NUMBER: US/10/268,051  
; CURRENT FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 60/328,464  
; PRIOR FILING DATE: 2001-10-11  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8

LENGTH: 1027

TYPE: PRT

ORGANISM: Squalus acanthias

US-10-268-051-8

Query Match 100.0%; Score 5410; DB 4; Length 1027;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLHCOLLFLGFTLLQSNVSGVGNQRAQKGDIIILGGLFPIHFGVAAKQDILKSRPE 60  
Db 1 MAQLHCOLLFLGFTLLQSNVSGVGNQRAQKGDIIILGGLFPIHFGVAAKQDILKSRPE 60  
QY 61 ATKIRYNFRGFWLQAMIFABEINNMTFLPNITLGYRIFDTCTNTVSKALEATLSFVA 120  
Db 61 ATKIRYNFRGFWLQAMIFABEINNMTFLPNITLGYRIFDTCTNTVSKALEATLSFVA 120  
QY 121 QNKIDSILNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSIASSSLLSN 180  
Db 121 QNKIDSILNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVSIASSSLLSN 180  
QY 181 KNEYKAFRLTIPNDEQQAATAMAEIIEHFQNNWVGTLLAADDYGRPGIDKFREEAVKRDIC 240  
Db 181 KNEYKAFRLTIPNDEQQAATAMAEIIEHFQNNWVGTLLAADDYGRPGIDKFREEAVKRDIC 240  
QY 241 IDESEMIQYITOKOLEFIADVIQNSAKVIVVFSNGPOLEPLIQHIVERNITDRIWLAS 300  
Db 241 IDESEMIQYITOKOLEFIADVIQNSAKVIVVFSNGPOLEPLIQHIVERNITDRIWLAS 300  
QY 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRI PGFNKFLKEVHPSSRSDNGFVKFEWEEFT 360  
Db 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRI PGFNKFLKEVHPSSRSDNGFVKFEWEEFT 360  
QY 361 NCYFTEKTLTQKNSKVPBGHGAAGDQSGKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420  
Db 361 NCYFTEKTLTQKNSKVPBGHGAAGDQSGKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420  
QY 421 HLRISVNVVAVYSIAHALQDIHSCKPGTGI FANGSCADIKKVEAWQVNLHLHLKFTNS 480  
Db 421 HLRISVNVVAVYSIAHALQDIHSCKPGTGI FANGSCADIKKVEAWQVNLHLHLKFTNS 480  
QY 481 MGEQVDFDQGDILKGNYYTIINWQSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILMSG 540  
Db 481 MGEQVDFDQGDILKGNYYTIINWQSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILMSG 540  
QY 541 FSKVVPFNSCRDCVPGTRKGIIEGPTCCFECMACAEGEFDENDASACTKCPNDFWSN 600  
Db 541 FSKVVPFNSCRDCVPGTRKGIIEGPTCCFECMACAEGEFDENDASACTKCPNDFWSN 600  
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY 660  
Db 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSFVLGVFIKFRNTPIVKATNRELSY 660  
QY 661 LLLFSLICCFSSSLIFIGEPDRWTCRLRQPAFGISFVLCISILVKTNRVLLVFEAKIPT 720  
Db 661 LLLFSLICCFSSSLIFIGEPDRWTCRLRQPAFGISFVLCISILVKTNRVLLVFEAKIPT 720  
QY 721 SLHRKWVGNLQFLVFLCILVQITVCIIWLTAPPSYRNHELEDEVIFITCDGSLMA 780  
Db 721 SLHRKWVGNLQFLVFLCILVQITVCIIWLTAPPSYRNHELEDEVIFITCDGSLMA 780  
QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFEAKFTFSNLFFIWMISFIPAYVSTYKGF 840  
Db 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFEAKFTFSNLFFIWMISFIPAYVSTYKGF 840  
QY 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900  
Db 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900  
QY 901 AASRKSSSLCGSTISSPASSTCGGLTMEMORCSTQKVSFGSGVTLSLFEETGRYAT 960  
Db 901 AASRKSSSLCGSTISSPASSTCGGLTMEMORCSTQKVSFGSGVTLSLFEETGRYAT 960



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QY 961 LSRTARSNSADGRSGDDLPSRHHDDQPPKCEPOPANDARYKAAPTGTLESPPGSKER 1020
DB 961 LSRTARSNSADGRSGDDLPSRHHDDQPPKCEPOPANDARYKAAPTGTLESPPGSKER 1020
QY 1021 PTTMEET 1027
DB 1021 PTTMEET 1027

RESULT 3
US-09-134-513-2
; Sequence 2, Application US/09134513
; Patent No. 6210964
; GENERAL INFORMATION:
; APPLICANT: Brown, Edward M.
; APPLICANT: Diaz, Ruben
; APPLICANT: Bai, Mei
; APPLICANT: Quinn, Stephen J.
; TITLE OF INVENTION: The Avian Extracellular Calcium-Sensing
; RECEPTOR
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Vinson & Elkins L.L.P.
; STREET: 1455 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20004-1008
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,513
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: BR1331/13003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)639-6585
; TELEFAX: (202)639-6604
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1059 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-134-513-2

Query Match 75.9%; Score 4106.5; DB 3; Length 1059;
Best Local Similarity 76.4%; Pred. No. 0;
Matches 788; Conservative 85; Mismatches 130; Indels 29; Gaps 5;

QY 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGDIIILGGLFPIHFGVAADQDLKS RPE 60
DB 1 MLYSCCLILLFT-----WNTRYGNQRAQKGDIIILGGLFPIHFGVAADQDLKS RPE 56
QY 61 ATKIRYNPRGRFWLQAMIFATEEINNMTFLPNITLGYRIPTDNTVSKALEATLSFVA 120
DB 57 SVECIYNPRGRFWLQAMIFATEEINNMTFLPNITLGYRIPTDNTVSKALEATLSFVA 116
QY 121 QNKIDSLNDEFNCNSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180
DB 117 QNKIDSLNDEFNCNSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 176
QY 181 KNEYKAFRLTIPNDEQATAMAEIIIEHFQWNNVGTLAADDYDGRFGIDKFREEAVKRDIC 240
DB 177 KNQFKSFLATIPNDEHQATAMADIIIEYFRWNVGTIAADDYDGRFGIEKFREEAEERDIC 236

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QY 241 IDSEMIQYTKQLEFIADVTIONSSAKVIVVFSNGPDLEPLIQEIVVRNITDRILWLAS 300
DB 237 IDSEMIQYSDSEBEEIQQVVEVIQNSTARVIVVSSGPDLEPLIKEIVVRNITGKIWLAS 296
QY 301 EAWASSSLIAKPEYFHVVGTTICFALRAGRIIFGFKFLKEVHPSRSDRGFKVEEFTF 360
DB 297 EAWASSSLIAMPEFFRVIGSTIGFALKAGQIPGFRFLOKVHPKSGANNKFAKEEFTF 356
QY 361 NCYFTEKTLTQKNKSKVPBGHPAAQDGGSKAGNSRTALRHPTCGEENITSETPYLDYT 420
DB 357 NCYLPSES-----KNSPASASFHKAHEGLGAGNG-TAAFRPPCTGDEENITSETPYMDFT 411
QY 421 HLRISYNYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAQVNLHLHLKFTNS 480
DB 412 HLRISYNYVAVYSIAHALQDIYTCYTGKGLFNGSCADIKKVEAQVNLKHLHLFTSN 471
QY 481 MGEQVDPDQDGLKGNYYIINWOLSAEDBSVLPHVEGNNYNAVAKPDRNINEKILLWSG 540
DB 472 MGEQVDPDEFGLVGNYSIINWHLSPEDGVSVPVEVGHYNNVYAKKGERLFINENKILLWSG 531
QY 541 FSKVVPSCNRDQVCPGTRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPNDFWSN 600
DB 532 FSKEVPSCNRDCLPGTRKGIIEGPTCCFECVDCPDGEISDETDASACDKCPEYWSN 591
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLIGILITSFVLGVFIKFRNTPIVKATNRELSY 660
DB 592 ENHTSCIPKQIEFLSWTEPFGIALTIFAVLIGILITSFVLGVFTKFRNTPIVKATNRELSY 651
QY 661 LLLPFLICPSSSLIFIGEPDWTCLRQPAFGISFVLCSILVKTNRVLLVFEAKIPT 720
DB 652 LLLPFLICPSSSLIFIGEPQNTCLRQPAFGISFVLCSILVKTNRVLLVFEAKIPT 711
QY 721 SLHRKWGLNLQFLVFLCIVLVOITCIWLYTAPSSYRNHELEDEVIPTCDEGSLMA 780
DB 712 SLHRKWGLNLQFLVFLCIVLVOITCIWLYTAPSSYRNHELEDEVIPTCDEGSLMA 771
QY 781 LGFLIGYTCLLAAICFFFAFKSKLPENFNEAKFITFSMLIFPIVWISPIPAVYSTYKGF 840
DB 772 LGFLIGYTCLLAAICFFFAFKSKLPENFNEAKFITFSMLIFPIVWISPIPAVYSTYKGF 831
QY 841 VSAVENTAILASSFGLLGCIVENKCVIILPKCRNTEIEVRCSTAAHAFKVAARATLRS 900
DB 832 VSAVENTAILAASFGLLGCIVENKCVIILPKCRNTEIEVRCSTAAHAFKVAARATLRS 891
QY 901 AASRKRSSSLCGSTISSPASSTCGPG-----LTMEMQRCSTQKVSGSGTGT 947
DB 892 NVSRKRNSLGGSTGSGTSSSISSKNHEDPFLPASAEQRQQRQCKQKVSGSGTGT 951
QY 948 LSLSPETGRYATLSRTARSNSADGRSGDDLPSRHHDDQPPKCEPOPANDARYKAAPT 1007
DB 952 LSLSPETGRYATLSRTARSNSADGRSGDDLPSRHHDDQPPKCEPOPANDARYKAAPT 1004
QY 1008 KGTLESPPGSGKE 1019
DB 1005 FQTASSPETSSQ 1016

RESULT 4
US-08-485-588-7
; Sequence 7, Application US/08485588
; Patent No. 5688938
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: Forrest H. Fuller
; APPLICANT: James E. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center

```

STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,588  
FILING DATE: 7 June, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: 9  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 213/005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1078 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-485-588-7

Query Match 74.6%; Score 4037.5; DB 1; Length 1078;  
Best Local Similarity 73.9%; Pred. No. 0;  
Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

QY 1 MAQLHCOLFLGFTLLQSNVSGYGNORAKKGDIILGGLFPFHFGVAAKQDLSRPE 60  
DB 1 MAFYSCCVLLALT-----WHTSAYGPDQRAKKGDIILGGLFPFHFGVAAKQDLSRPE 56  
QY 61 ATKIRYNRGRFWLQAMIFAEIEINNSMTFLPNTTLGYRIFDTCNTVSKALEATLSVA 120  
DB 57 SVECIYNRGRFWLQAMIFAEIEINNSPALLPNTTLGYRIFDTCNTVSKALEATLSVA 116  
QY 121 QNKIDSLNDEFNCNSDHPSTPIAVVATGSGISTAVANLLGLFVPOVSASSRLLSN 180  
DB 117 QNKIDSLNDEFNCNSHSPSTPIAVVATGSGISTAVANLLGLFVPOVSASSRLLSN 176  
QY 181 KNEYKAFRTIPNDEQQATAMAEIIEHFQWNVVGTAAADDDYGRPGIDKFREEAVKRDIC 240  
DB 177 KNQFKSFLRTIPNDEHQATAMADIEYFRWNVVGTAAADDDYGRPGIEKFREEAEERDIC 236  
QY 241 IDPSEWISQYTKQLEPTADVIQNSAKVIVVFNFGPDLEPLQEIIVRNITDRILAS 300

DB 237 IDFSELISQYSDDEEIQHVVEIQNSTAKVIVVFNFGPDLEPLQEIIVRNITDRILAS 296  
QY 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPOFNKFLKEVHPSRSDGFGVKEFEETFF 360  
DB 297 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPOFNKFLKEVHPSRSDGFGVKEFEETFF 356  
QY 361 NCYFTEKTLTQKNKVPKSHGPAAGQDGGKAGNSRRATLRHPCTGBENTTSVETPTLDYT 420  
DB 357 NCHLOEGAKGPL---PVDTFLRGHESGDRFNS-STARPLCTGDNSSVETPTLDYT 412  
QY 421 HLRISYVYVAVYSIAHALODIHSCKPGTGI FANGSCADIKKVEAWQVNLHLHLKFTNS 480  
DB 413 HLRISYVYVAVYSIAHALQDIYTCPLPGRGLFTNGSCADIKKVEAWQVNLHLHLNFTNN 472  
QY 481 MGEQVDFDDGDLKGNVTIINWOLSAEDBSVLPHVEVGNVYAKPSDRNLNINEKKILWSG 540  
DB 473 MGEQVDFDECDLVGNYSIINWHLSPEDGSI FKEVGYVYVYAKKGERLFINEKILWSG 532  
QY 541 FSKVVPFNSCRDVCVPTGRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPNDFWSN 600  
DB 533 FSREVPFNSCRDCLAGTRKGIIEGPTCCFECVCEPDGGEYSDETDASACNKPDPFWSN 592  
QY 601 ENHTSCIATKEIEVLSWTEPGIATTFIVLGLITTSVLGVFTKFRNTPIVKATNRELSY 660  
DB 593 ENHTSCIATKEIEFLSWTEPGIATTFIVLGLITTSVLGVFTKFRNTPIVKATNRELSY 652  
QY 661 LLLFSLTCCFSSSLIFIGBPRDWTCLRQPAFGISFVLGICILVKTNRVLLVFEAKIPT 720  
DB 653 LLLFSLTCCFSSSLIFIGBPRDWTCLRQPAFGISFVLGICILVKTNRVLLVFEAKIPT 712  
QY 721 SLHRKVVGLNLQFLVFLCIVLQIVTCIWLTPAPSSYANHELEDEVIFITCDEGSLMA 780  
DB 713 SFHRKVVGLNLQFLVFLCIVLQIVTCIWLTPAPSSYANHELEDEVIFITCDEGSLMA 772  
QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFVWISFIPAYVSTYGF 840  
DB 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFVWISFIPAYVSTYGF 832  
QY 841 VSAVEVIALASSGGLLCIYFNKCVIILFKPCRNTEIIVRCSTAAHAFKVAARATLRS 900  
DB 833 VSAVEVIALASSGGLLCIYFNKCVIILFKPCRNTEIIVRCSTAAHAFKVAARATLRS 892  
QY 901 AASRKSSSLCGSTISSPASSTCGPG-----LTMEM 931  
DB 893 NVSRKSSSLGSGTSGTSPSSSSSKNSNEDPPFQPERQKQOQPLALTQOQOQPLTLPQ 952  
QY 932 Q-----RCSTOKVSFGSTVLSLSEETGRYATLSRTARSNSADGRSGDDLPSSRH 984  
DB 953 QORSQOQPRCK-QKVIFFSGTFTFSLSFDEPOKNAHAGNSTHONSLEAKQSDDLTRH- 1010  
QY 985 DQSPKCKEPOPANDARYKAAPTKLTLESPPGSKERP 1021  
DB 1011 -----QPLFLQCGTDLTLTVOETGLQGPVGDDQRP 1042  
RESULT 5  
US-08-484-565-7  
Sequence 7, Application US/08/484565  
Patent No. 5763569  
GENERAL INFORMATION:  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles

STATE, California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,565  
FILING DATE: 7 June, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below: 9  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 213/006  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1078 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-565-7

Query Match 74.6%; Score 4037.5; DB 1; Length 1078;  
Best Local Similarity 73.9%; Pred. No. 0;  
Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

QY 1 MAOLHCOLLFLGFTLLQSNVSGYGNQRAQKGDIIILGGLFPIHFGVAADODLKS RPE 60  
DB 1 MAFYSCCWVLLALT---WHTSAYGPDQAQKGDIIILGGLFPIHFGVAADODLKS RPE 56  
QY 61 ATKCIYRNGRFRWLQAMIFAIEEINNGMTFLPNITLGYRIPDTCNTVSKALEATLSFVA 120  
DB 57 SVECIYRNGRFRWLQAMIFAIEEINSSPALLNLTGLYRIPDTCNTVSKALEATLSFVA 116  
QY 121 QNKIDSLNDECNCSDHIPSTIAVVGATSGISTAVANLGLFYIPOVYASSSRLLSN 180  
DB 117 QNKIDSLNDEFCNCSSEHIPSTIAVVGATSGVSTAVANLGLFYIPOVYASSSRLLSN 176  
QY 181 KNEYKAFRLTIINDEQATAMAEIIHFQWNVVGTAAADDDYGRFGIDKFREEAVKRDIC 240  
DB 177 KNQKSFRLTIINDEHQATAMADIIIFYFNNVWVGIIAADDYGRFGIEKFREEAEERDIC 236  
QY 241 IDFSEWISQYTKOLEFTADVIONSSAKVIIVFNGDPLELQIEIVRRNITDRINWLAS 300  
DB 237 IDFSELISQYSEERIOHVVEIQNSTAKVIIVFSSGPDLEPLIKEIVRRNITGKIWLAS 296

QY 301 EAWASSLLIAKPEYFHVVGTTIGFALRAGRIPGFNKFLKEVHPSRSSDNGFVKFEWEETF 360  
DB 297 EAWASSLLIAKPEYFHVVGTTIGFALRAGRIPGFRFLKKVHPRKSVHNGFAKFEWEETF 356  
QY 361 NCYFTEKTLTQLNKSKVPBGHGAAGDGGKAGNSRRATLHPTGCTGSENTISVETPYLDYT 420  
DB 357 NCHLQEGAKGPL---PVDTFRLRGHEESGDRFNS--STAFLPLCTGDENISSVETPYIDYT 412  
QY 421 HLRISYNNVAVYSIAHALODIHSOKPGTGIIFANGSCADIKKVEAQVNLHLLHLKFTNS 480  
DB 413 HLRISYNNVAVYSIAHALQDIYITCLPGRGLFTNGSCADIKKVEAQVNLHLLHLNFTNW 472  
QY 481 MGEQVDFDQDGLKGNYYTIINWOLSAEDSVLFHEVGYNNAYAKPSDRININEKILWSG 540  
DB 473 MGEQVDFDECGDLVGNYSIINWHLSPEDGSIIVFEKVGYYNVYAKKGERLFINEEKILWSG 532  
QY 541 FSKVPFNSCSDRCVFGTRKGIIEGPTCCFECMACAEFGSDENDASACTKCPNDFWN 600  
DB 533 FSREVPFNSCSDCLAGTRKGIIEGPTCCFECVCEPCDGEYSDETDASACNCPDDFWN 592  
QY 601 ENHTSCIAKIEYLSWTEPFEGIALTIFAVLGILITISFVLGVPIKFRNTPIVKATNRELSY 660  
DB 593 ENHTSCIAKIEYLSWTEPFEGIALTIFAVLGILITISFVLGVPIKFRNTPIVKATNRELSY 652  
QY 661 LLLFSLICPSSSLITIGEPDWTCLROPAGISVLCISLILVKTNRVLLVFEAKIPT 720  
DB 653 LLLFSLICPSSSLITIGEPDWTCLROPAGISVLCISLILVKTNRVLLVFEAKIPT 712  
QY 721 SLHRKXWGLNLQFLVFLCIILOVITCIITWLYTAPSSYRNHELEDEVIFITCEGSLMA 780  
DB 713 SFHRKXWGLNLQFLVFLCIILOVITCIITWLYTAPSSYRNHELEDEVIFITCEGSLMA 772  
QY 781 LGFLIGYTCLLAAICFFFAFKSKLPENFNEAKFITFMSLIFFIVWISFIPAYVSTYKGF 840  
DB 773 LGFLIGYTCLLAAICFFFAFKSKLPENFNEAKFITFMSLIFFIVWISFIPAYVSTYKGF 832  
QY 841 VSAVEVIAIILASSFGLLCIYFNKCVIILPKPCNTIEEVRCSTAAHAFKVAARATLRS 900  
DB 833 VSAVEVIAIILASSFGLLCIYFNKCVIILPKPCNTIEEVRCSTAAHAFKVAARATLRS 892  
QY 901 AASKRSSSLCGSTISSPASSTCGPG-----LTMEM 931  
DB 893 NVSRKSSSLGGSTGTSTPSSSISSKNSNEDPFPQPERKQOQPLALTQOQOQPLTLQ 952  
QY 932 Q-----RCSTOKVSGGTVTLSISFEETGYATLSRTARSRNADGRSGDDLSRHH 984  
DB 953 QORSQOQPRCK-QKVIIFSGGTVTLSISFDEPQKNAMAHGNSTHNSLEAQKSDTLTRH- 1010  
QY 985 DQPPKCEPQANDARYKAAPTGTLESFGGSKERP 1021  
DB 1011 -----QPLLPQCGEITDLDLTVQETGLQGPVGGQRP 1042

RESULT 6  
US-08-480-751-7  
Sequence 7, Application US/08480751  
Patent No. 585684  
GENERAL INFORMATION:  
APPLICANT: Edward F. Nemeth  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
APPLICANT: Forrest H. Fuller  
APPLICANT: James E. Garrett, Jr.  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California

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COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-480-751-7

Query Match 74.6%; Score 4037.5; DB 2; Length 1078;
Best Local Similarity 73.9%; Pred. No. 0;
Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

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DB 117 QNKIDSLNLFDFCNCSEHPTPIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 176
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DB 177 KNOQSFSLRTIENDEHQATAMADIIEYFRWNVGTAAADDDYGRGIDKPFREAVKRDIC 236
QY 241 IDPSEWISQYTKOLEFTADYQNSAKVIVFNSGPDLEPLIOEIVVRNITDRIWLAS 300
DB 237 IDPSELISQYSEEBEQHVVEIQNSTAKVIVFSSGPDLEPLIOEIVVRNITDRIWLAS 296
QY 301 EAWASSSLIAKPEYFHVVGTTGFALRAGRIPGFNFKFLKEVHPSPSSDNGFVKFEWETF 360

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QY 361 NCYFTEKTLTQLNKSKVPSPHGAQGGKAGNSRRTALRHPTGBENITSVETPYLDT 420
DB 357 NCHLQEGAKGFL--PVDFTLRGHBESGDRFNS--STAFRPLCTGDNISSEVETPYDIT 412
QY 421 HLRISYVYVAVYSIAHALQDIHSCKPGTCIFANGSCADIKKVEAWQVNLHLHLKFTNS 480
DB 413 HLRISYVYVAVYSIAHALQDIHSCKPGTCIFANGSCADIKKVEAWQVNLHLHLKFTNS 472
QY 481 MGEQVDFDDQGLKGNYYTINWOLSAEDSVLFEHVGNYNAYAKPSDRNLNINEKKILWSG 540
DB 473 MGEQVDFDDQGLKGNYYTINWOLSAEDSVLFEHVGNYNAYAKPSDRNLNINEKKILWSG 532
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DB 533 FSKVVPFSCNRDVCVPTKGIIEGPTCCFECMACAEGEFSDENDASACTCPNDFWN 592
QY 601 ENHTSCIATKIEIYLSWTEPFEGIALTIFAVLGIILITFVLGVFIKFRNTPIVKATNRELSY 660
DB 593 ENHTSCIATKIEIYLSWTEPFEGIALTIFAVLGIILITFVLGVFIKFRNTPIVKATNRELSY 652
QY 661 LLLFSLICFSSSLIFIGBPRDWTCLROPAGISFVLICISLILVKTNRVLLVFEAKIPT 720
DB 653 LLLFSLICFSSSLIFIGBPRDWTCLROPAGISFVLICISLILVKTNRVLLVFEAKIPT 712
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DB 713 SLHRKWGLNLQFLVFLCIILOVITCIWLTAPPSSYRNHELEDEVIFITCDEGSLMA 772
QY 781 LGFLIGYTCLLAAICFFFAFKSKLPENFNKAITFMSLIIFFIIVWISIPAYVSTYKGF 840
DB 773 LGFLIGYTCLLAAICFFFAFKSKLPENFNKAITFMSLIIFFIIVWISIPAYVSTYKGF 832
QY 841 VSAVEVITALLASSFGLIGCIYFNKCVIILFKPCRNTEIEVRCSTAHAHFKVAARATLRS 900
DB 833 VSAVEVITALLASSFGLIGCIYFNKCVIILFKPCRNTEIEVRCSTAHAHFKVAARATLRS 892
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QY 932 Q-----RCSTOKVSFGSTVTLISLFEETGYATLSRTARSNADGRSGDGLPSRHH 984
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DB 1011 -----QPLLPLOQGETDLDLTQVETGLQGVGQDQRP 1042

RESULT 7
US-08-943-986-7
Sequence 7, Application US/08943986
Patent No. 5962314
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:

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SOFTWARE: FastSeq for Windows Version 3.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,719B  
FILING DATE: 7 June, 1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994  
APPLICATION NUMBER: U.S. 08/292,827  
FILING DATE: 23 August, 1994  
APPLICATION NUMBER: U.S. 08/141,248  
FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Douglas C. Murodock  
REGISTRATION NUMBER: 37,549  
REFERENCE/DOCKET NUMBER: 213/007  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1078 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-484-719B-7

Query Match 74.6%; Score 4037.5; DB 3; Length 1078;  
Best Local Similarity 73.9%; Pred. No. 0;  
Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

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Db 57 SVECIKYNFRGRFWLQAMIFATEEINNSPALLPNTTLGVRIFDTCNTVSKALEATLSVA 116  
QY 121 QNKIDSLNLDFCNCSDHIPSTIAVVGATGSGISTAVANLGLFYIPQVSVASSRLLSN 180  
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QY 241 IDFSEMIQYTKQLEFIADYQNSAKVIIVFSGNPDLEPLIOEIVRRNITRILWLAS 300  
Db 237 IDFSELIQSYDEEIQHVVEIQNSTAKVIIVFSSGPDLEPLIKEIVRRNITGKIWLAS 296  
QY 301 EAWASSLIAPKPEYFHVVGTTGFMALRAGRIPGNFKLKEVHPSSSSNGFVKFWEETP 360  
Db 297 EAWASSSLIAMPQYFHVVGTTGFMALRAGRIPGNFKLKEVHPSSSVHNGFAKFEETP 356  
QY 361 NCYFTEKTLTOLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420  
Db 357 NCHLQEGAGPL---PVDTFLRGHEESGDRFSNS-STAFRPLCTGDENISSVEIPYIDYT 412

421 HLRISNVYVAVYSIAHALQDIHSCRPGTGIFANGSCADIKKVEAWQVLNHLHLKFTNS 480  
Db 413 HLRISNVYVAVYSIAHALQDIYTCPLGRGLFTNGSCADIKKVEAWQVLKHLRLAFTNN 472  
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Db 473 MGEQVTFDECGDLVGNYSIINWLSPEDESVIVFKEVGNVNAKGRULFINKEKILMSG 532  
QY 541 FSKVVPFNSCNRDCVPTGRKGIIEGEPTECCFECMACAEGEFSDENDASACTKCPNDPWSN 600  
Db 533 FSREVFPNSCNRDCLAGTRKGIIEGEPTECCFECVECPDGEYSDETDASACNKCDDFSWN 592  
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Db 593 ENHTSCIAKEIEFSLWTEPPGIALTIIPAVLGIILITSFVLGVFKFRNTTIVKATNEELSY 652  
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Db 653 LLLFSLICCPSSSLIFIGBRDWTCLROPAGFISVLCISCLIVKTNVLLVFEAKIPT 712  
QY 721 SLHRKWGLNLQFLVLCILVQIVTCIILWYTPAPSSYRNHELEDEVIFITCDEGSLMA 780  
Db 713 SPHRKWGLNLQFLVLCILVQIVTCIILWYTPAPSSYRNHELEDEVIFITCDEGSLMA 772  
QY 781 LGFLIGYTCLLAAICFFFAKSKLPENENAKFITFMSLIPFIVATSFIPAYVSTYKGF 840  
Db 773 LGFLIGYTCLLAAICFFFAKSKLPENENAKFITFMSLIPFIVATSFIPAYVSTYKGF 832  
QY 841 VSAVEVIAILASSFGLIGCIYFNKCVIILFKPCNTIEEVRCSTAAHAFKVAARATLRRS 900  
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QY 932 Q-----RCSTQKVGSGTIVTSLSFETGYATLSRTARSRNSADGRSGDDLPSSRH 984  
Db 953 QORSQOQPRCK-QKVFSGTIVTSLSFETGYATLSRTARSRNSADGRSGDDLPSSRH 984  
QY 985 DQPPQKCEPQANDARYKAAPTKGTLESFGSGSKERP 1021  
Db 1011 -----QPLLPQCGETDLDLTVOETGLQGVGGDQRP 1042

RESULT 10  
US-08-484-159-7  
Sequence 7, Application US/08484159  
Patent No. 6313146  
GENERAL INFORMATION:  
APPLICANT: Bradford C. Van Wagenen  
APPLICANT: Manuel P. Balandrin  
APPLICANT: Eric G. Del Mar  
APPLICANT: Edward F. Nemeth  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,159

[illegible]

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; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9
; APPLICATION NUMBER: 08/353,784
; FILING DATE: 9 December, 1994
; APPLICATION NUMBER: PCT/US/94/12117
; FILING DATE: 21 October, 1994
; APPLICATION NUMBER: U.S. 08/292,827
; FILING DATE: 23 August, 1994
; APPLICATION NUMBER: U.S. 08/141,248
; FILING DATE: 22 October, 1993
; APPLICATION NUMBER: U.S. 08/009,389
; FILING DATE: 23 February, 1993
; APPLICATION NUMBER: U.S. 08/017,127
; FILING DATE: 12 February, 1993
; APPLICATION NUMBER: U.S. 07/934,161
; FILING DATE: 21 August, 1992
; APPLICATION NUMBER: U.S. 07/834,044
; FILING DATE: 11 February, 1992
; APPLICATION NUMBER: U.S. 07/749,451
; FILING DATE: 23 August, 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon C.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 213/005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1088 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-588-6

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Query Match 74.5%; Score 4029.5; DB 1; Length 1088;
Best Local Similarity 73.3%; Pred. No. 0;
Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;

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DB 1 MAFYSCCVLLALT----WHTSAYGQDQRAKKGGIILGGLPHHFGVAAKQDQLKSRPE 56
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956 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
957 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
958 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
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961 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
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965 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
966 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
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970 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
971 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
972 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
973 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
974 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
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979 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
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986 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
987 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
988 FSK-----VWPFNSCSRDVPGTRKGIIBGEPTCCFECMACAEGEFSDENDASAC 592
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RESULT 12
US-08-484-565-6
; Sequence 6, Application US/08484565
; Patent No. 5763569
; GENERAL INFORMATION:
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; APPLICANT: James R. Garrett, Jr.
; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: First Interstate World Center
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FASTSEQ
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,565
; FILING DATE: 7 June, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: 9

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533 FSREPLTVLSVLQVFNCSRDCLAGTRKGIIEGPTCCFECVCEPCDEYSDETDASAC 592  
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593 NKCPDDFWNSNHTSCIAKEIEFLSWTEPFGIALTIFAVLGLIFLTAFLVGLGVFIKPRNTPI 552  
651 VKATNRELSVLLFLSLICCFSSSLIFIGEPDWTCLROPATGISFVLCISILVKTNRV 710  
653 VKATNRELSVLLFLSLICCFSSSLIFIGEPDWTCLROPATGISFVLCISILVKTNRV 712  
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713 LLVFEAKIPTSLHRKWVGLNQLFLLVFLCILVQIVTCIIWLVTAPSSVYRNHELEDEVIF 772  
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773 ITCEGSLMALGFLIGYTCLLAACFFPAFKSRKLPENNEAKFITFSLMIFLVIWISFI 832  
831 PAYVSTYGVKFSVAVEVIALASSFGLLGCIFYFNKCYIILFKPCRNTEIEVRCSTAAHAFK 890  
833 PAYASTYGVKFSVAVEVIALASSFGLLGCIFYFNKCYIILFKPCRNTEIEVRCSTAAHAFK 892  
891 VAARATLRRSAASKRKSLSLGGSTISSPASSTCGPG----- 926  
893 VAARATLRRSNVSRKRSLSLGGSTISSPASSTISKSNSEDPFPRPERKQOQPLALTQOE 952  
927 -----LTMEMQ-----RCSTOKVSFGSTVLSLFEETGRYATLSRTARSNSADGR 974  
953 QOQOPLTLPOQRSQOQPRCK-OKVLFSGTIVTSLFDEPQKNANVAHNSHTQNSLEAQ 1011  
975 SGDDLFSRHHDOGPQKCEPQANDARYKAAPTKGTLESPPGSGKERP 1021  
1012 KSSDTLTRH-----QPLLPLOQGETDLTLVQETGLQGVGVDQRP 1052

RESULT 14  
US-08-943-986-6  
Sequence 6, Application US/08943986  
Patent No. 5962314  
GENERAL INFORMATION:  
APPLICANT: Edward M. Brown  
APPLICANT: Steven C. Hebert  
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
TITLE OF INVENTION: MOLECULES  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: First Interstate World Center  
STREET: Suite 4700  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: FASTSEQ  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,986  
FILING DATE: 03-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/484,565  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: 08/353,784  
FILING DATE: 9 December, 1994  
APPLICATION NUMBER: PCT/US/94/12117  
FILING DATE: 21 October, 1994

541 FSK-----VVPFNSCRDVCPTGTRKGIIEGPTCCFECMACAEGEFSDENDASAC 590  
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593 NKCPDDFWNSNHTSCIAKEIEFLSWTEPFGIALTIFAVLGLIFLTAFLVGLGVFIKPRNTPI 552  
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1012 KSSDTLTRH-----QPLLPLOQGETDLTLVQETGLQGVGVDQRP 1052

Query Match 74.5%; Score 4029.5; DB 2; Length 1088;  
Best Local Similarity 73.3%; Pred. No. 0;  
Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;  
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301 EAWASSSLIAKPEYFHVVGGTIGFALRAGRIPOFNKFLKEVHPFSRSDNGPFVKEFEWETF 360  
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413 HLRISYVAVYVSIHAHQDIHSCKPGTGIFANGSCADIKKEVQWVNLHLLHLLKFTNS 472  
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473 MGEQVTFDECDLVGNYSIINWHLSPEDGSIYFKEVGYVNVYAKGERLFINEEKILMSG 532

APPLICATION NUMBER: U.S. 08/292,827  
 FILING DATE: 23 August, 1994  
 APPLICATION NUMBER: U.S. 08/141,248  
 FILING DATE: 22 October, 1993  
 APPLICATION NUMBER: U.S. 08/009,389  
 FILING DATE: 23 February, 1993  
 APPLICATION NUMBER: U.S. 08/017,127  
 FILING DATE: 12 February, 1993  
 APPLICATION NUMBER: U.S. 07/934,161  
 FILING DATE: 21 August, 1992  
 APPLICATION NUMBER: U.S. 07/834,044  
 FILING DATE: 11 February, 1992  
 APPLICATION NUMBER: U.S. 07/749,451  
 FILING DATE: 23 August, 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Heber, Sheldon O.  
 REGISTRATION NUMBER: 38,179  
 REFERENCE/DOCKET NUMBER: 213/006  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1088 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-943-986-6

Query Match 74.5%; Score 4029.5; DB 2; Length 1088;  
 Best Local Similarity 73.3%; Pred. No. 0;  
 Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;

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 413 HLRISVNVVAVYSTAHALQDIHSCKPGTGFANGSCADIKKVEAWQVNLHLLKFTNS 472  
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 593 NKCPDDFWSNENHTSCIAKEIYLSWTEPFGIALTIFAVLGILITSPVLGVFKFNTPI 652  
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 713 LLYPEAKIPTSFHRKXVGLNQLLVLCLLVQIVTCIILWLYTAPSSYRNHELEDEVIF 772  
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 833 PAYASTYCKTVSAVEVIAIILASSFGLLGCYFNKCVIILFKPCORNTIEVRCSTAAHAFK 892  
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 1012 KSSDTLTH-----QPLLPQCGETDLTLTVOETGLQGPVGQDQRP 1052

RESULT 15  
 US-08-353-784-6  
 ; Sequence 6, Application US/08353784  
 ; Patent No. 6011068  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Edward F. Nemeth, Edward M.  
 ; APPLICANT: Brown, Steven C. Hebert,  
 ; APPLICANT: Bradford C. Van Wagenen, Manuel  
 ; APPLICANT: F. Balandrin, Forrest H. Fuller,  
 ; APPLICANT: Eric G. DelMar, and Scott T. Moe  
 ; TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE  
 ; TITLE OF INVENTION: MOLECULES  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: First Interstate World Center  
 ; STREET: Suite 4700  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: FASTSEQ  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/353,784  
 ; FILING DATE: 9 December, 1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; PRIOR APPLICATION DATA: including application  
 ; PRIOR APPLICATION DATA: described below: B  
 ; APPLICATION NUMBER: PCT/US/94/12117  
 ; FILING DATE: 21 October, 1994  
 ; APPLICATION NUMBER: U.S. 08/292,827  
 ; FILING DATE: 23 August, 1994  
 ; APPLICATION NUMBER: U.S. 08/141,248



FILING DATE: 22 October, 1993  
APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 209/069  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1088 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-353-784-6

Query Match 74.5%; Score 4029.5; DB 3; Length 1088;  
Best Local Similarity 73.3%; Pred. No. 0;  
Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;

Qy 1 MAQLHCQLLFIQFTLLQSNVSGYGNQRAQKGGIILGLGFPPIHFGVAAXDQDLKSPE 60  
Db 1 MAFYSCCWVLLALT---WHTSAYGPDQRAQKGGIILGLGFPPIHFGVAAXDQDLKSPE 56  
Qy 61 ATKCRYNRGRFRWLQAMFAIEEENNSMTFLPNTITLGYRIFDTCNTVSKALEATLSFVA 120  
Db 57 SVECTRYNFRGRWLQAMFAIEEENNSPALPNTITLGYRIFDTCNTVSKALEATLSFVA 116  
Qy 121 QNKIDSLNLDPCNCSGDIHPISTIAVVGATGSGISTAVANLGLFYIPOVSYASSRLLSN 180  
Db 117 QNKIDSLNLDPCNCSGDIHPISTIAVVGATGSGISTAVANLGLFYIPOVSYASSRLLSN 176  
Qy 181 KNEYKAFRTIENDEQATAMAEIIEHPQWNVGTLAADDYGRPGIDKFREEAVKRDIC 240  
Db 177 KNQFSLRTIENDEQATAMADIIEYFAWNVGTLAADDYGRPGIDKFREEAERDIC 236  
Qy 241 IDFSEMIQYTTQKLEFIADYQNSAKVIYVFSNGPDLEPLIQEIVRRNITDRIWLAS 300  
Db 237 IDFSELIQYSDDEBIQHVVEIQNSTAKVIYVFSNGPDLEPLIKIIVRRNITGKIWLAS 296  
Qy 301 EAWASSLIATKPEYHVVCGTIGFALRAGRIIPGNKFLKEVHPSSSDNGFVKEFEWETF 360  
Db 297 EAWASSLIAMPQYFHVVGTTIGFALKAGQIPGFREFLKKVHPKSVHNGFAKEFEWETF 356  
Qy 361 NCVFTEKTLTQKNKVPSPGHPAAQDGSKAGNSRRTRLRHPCTGEENITSVETPYLDYT 420  
Db 357 NCHLQEGAKPL--PVDIFLRGHEBSGDRFSNS-STAFRPLCTGDNISSVETPYIDYT 412  
Qy 421 HLRISYNTVAVYSIAHALQDTHSCKPGTGIIFANGSCADIKKVEAWQVNLHLHLKFTNS 480  
Db 413 HLRISYNTVAVYSIAHALQDIYTCPLPGRGLEFNGSCADIKKVEAWQVNLHLHLNFTNN 472  
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Qy 591 TKCPDQFWSNENHTSCIATIEYLSWTEPFGIALTIFAVLGIETLFAVLGVFIKFRNTPI 650  
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Qy 651 VKATNRELSYLLLFSLICCFSSSLIIFIGEPDWTCLRQPAFGISFVLCISILVKTNRV 710  
Db 653 VKATNRELSYLLLFSLICCFSSSLIIFIGEPDWTCLRQPAFGISFVLCISILVKTNRV 712  
Qy 711 LLVFEAKIPTSLHRKWKVGLNLQFLLVFLCILLVQIVTICIIWLITAPDSSYRNHELEDEVIF 770  
Db 713 LLVFEAKIPTSFHRKWKVGLNLQFLLVFLCITFMQIVICVWLITAPDSSYRNQLEDEIIF 772  
Qy 771 ITCDGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFFIVWISFI 830  
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APPLICATION NUMBER: U.S. 08/009,389  
FILING DATE: 23 February, 1993  
APPLICATION NUMBER: U.S. 08/017,127  
FILING DATE: 12 February, 1993  
APPLICATION NUMBER: U.S. 07/934,161  
FILING DATE: 21 August, 1992  
APPLICATION NUMBER: U.S. 07/834,044  
FILING DATE: 11 February, 1992  
APPLICATION NUMBER: U.S. 07/749,451  
FILING DATE: 23 August, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 209/069  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1088 amino acids  
TYPE: amino acid  
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MOLECULE TYPE: protein  
US-08-353-784-6

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ALIGNMENTS

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; Sequence 2, Application US/10125792  
; Publication No. US20030051269A1  
; GENERAL INFORMATION:  
; APPLICANT: MariCal  
; APPLICANT: Harris, H. William  
; APPLICANT: Betka, Marlies  
; APPLICANT: Nearing, Jacqueline A.  
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
; FILE REFERENCE: 2213.1006-007  
; CURRENT FILING DATE: 2002-08-16  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR FILING DATE: 2001-10-11  
; PRIOR FILING DATE: 2000-10-12  
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; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1027  
; TYPE: PRT  
; ORGANISM: Squalus acanthias  
US-10-125-792-2

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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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4	5410	100.0	1027	14	US-10-125-772-2
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8	4044.5	74.8	1078	14	US-10-159-339-8
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RESULT 2

US-10-125-778-2

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; Publication No. US20030082574A1
; GENERAL INFORMATION:
; APPLICANT: MariCal
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213.1006-005
; CURRENT APPLICATION NUMBER: US/10/125.778
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 10/121.441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240.392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240.003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Squalus acanthias
US-10-125-778-2

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Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Harris, H. William
; APPLICANT: Jury, Steven
; APPLICANT: Russell, David R.
; APPLICANT: Nearing, Jacqueline A
; APPLICANT: Betka, Marlies
; APPLICANT: Linley, Timothy
; APPLICANT: Brown, Edward M
; TITLE OF INVENTION: Methods for Growing and Imprinting Fish Using an Odorant
; FILE REFERENCE: 2213 2004-001
; CURRENT APPLICATION NUMBER: US/10/268,051
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/328,464
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Squalus acanthias
US-10-268-051-8

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 541 FSKVVPFNSRDCVPGTRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPNDFWSN 600
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITISFVLGVFIKFRNTPIVKATNRELSY 660
DB 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITISFVLGVFIKFRNTPIVKATNRELSY 660
QY 661 LLLFSLICFSSSLIFIGEPDWTCLRQAPAGISFVLCISILVKTNRVLLVFEAKIPT 720
DB 661 LLLFSLICFSSSLIFIGEPDWTCLRQAPAGISFVLCISILVKTNRVLLVFEAKIPT 720
QY 721 SLHRKWGLNQLFLLVFLCIIQIVTCIILWLTAPSSYRNHELEDEVIPTCDEGSLMA 780
DB 721 SLHRKWGLNQLFLLVFLCIIQIVTCIILWLTAPSSYRNHELEDEVIPTCDEGSLMA 780
QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLFFIIVWISFIPAYVSTYKGF 840
DB 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLFFIIVWISFIPAYVSTYKGF 840
QY 841 VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
DB 841 VSAVEVIAILASSFGLGCIYENKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900
QY 901 AASRRSSSLCGSTISSPASSTCGGLTWMORCSTQKVSFGSGVTLSLFEETGRYAT 960
DB 901 AASRRSSSLCGSTISSPASSTCGGLTWMORCSTQKVSFGSGVTLSLFEETGRYAT 960
QY 961 LSRTARSRNSADGRSGDDLPSRHHQGGPPQKCEPOPANDARYKAAPTKGTLESFGSKER 1020
DB 961 LSRTARSRNSADGRSGDDLPSRHHQGGPPQKCEPOPANDARYKAAPTKGTLESFGSKER 1020
QY 1021 PTTMEET 1027
DB 1021 PTTMEET 1027

RESULT 4
US-10-125-772-2
; Sequence 2, Application US/10125772
; Publication No. US20030124657A1
; GENERAL INFORMATION:
; APPLICANT: Marical
; APPLICANT: Harris, H. William
; APPLICANT: Nearing, Jacqueline A.
; APPLICANT: Betka, Marlies
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon
; FILE REFERENCE: 2213 1006-006
; CURRENT APPLICATION NUMBER: US/10/125,772
; CURRENT FILING DATE: 2002-08-16

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; PRIOR APPLICATION NUMBER: 10/121,441
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US01/31704
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/240,392
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: 60/240,003
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Squalus acanthias
US-10-125-772-2

Query Match      100.0%; Score 5410; DB 14; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKDQDLKSRE 60
DB 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKDQDLKSRE 60
QY 61 ATKCIYRNFRGFWLQAMFAIEEINNMTFLPNITLGYRIEDTCTNTVSKALEATLSFVA 120
DB 61 ATKCIYRNFRGFWLQAMFAIEEINNMTFLPNITLGYRIEDTCTNTVSKALEATLSFVA 120
QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYPOVSYASSRLLSN 180
DB 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYPOVSYASSRLLSN 180
QY 181 KNEYKAFPLTIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRPGIDKFEAEVKRDI 240
DB 181 KNEYKAFPLTIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRPGIDKFEAEVKRDI 240
QY 241 IDPSEMISQYTKQLEFIADVIQNSAKVIVVFNNGDPLELIQEIIVRNITDRIWLAS 300
DB 241 IDPSEMISQYTKQLEFIADVIQNSAKVIVVFNNGDPLELIQEIIVRNITDRIWLAS 300
QY 301 EAWASSLLAKPEYFHVVGTTGFAIRAGRIEFGNKFKEVHPSRSSDNGFVKFEWETP 360
DB 301 EAWASSLLAKPEYFHVVGTTGFAIRAGRIEFGNKFKEVHPSRSSDNGFVKFEWETP 360
QY 361 NCYFTEKTLTQKNSKVPBGHGAQDGSGKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420
DB 361 NCYFTEKTLTQKNSKVPBGHGAQDGSGKAGNSRRRTALRHPCTGEENITSVETPYLDYT 420
QY 421 HLRISYNNVAVYSTAHALQDTHSKPGTGIIFANGSCADIKKVEAMQVNLHLHLKFTNS 480
DB 421 HLRISYNNVAVYSTAHALQDTHSKPGTGIIFANGSCADIKKVEAMQVNLHLHLKFTNS 480
QY 481 MGEQVDFDQDGLKGNVTIINNQLSAEDSVLFHEVGNVNAKPSDRNLNINEKKILMSG 540
DB 481 MGEQVDFDQDGLKGNVTIINNQLSAEDSVLFHEVGNVNAKPSDRNLNINEKKILMSG 540
QY 541 FSKVPFNSCSDRCPVGTGKIIEBPTCCFPCMAEFGSDENDASACTKCPNDPWSN 600
DB 541 FSKVPFNSCSDRCPVGTGKIIEBPTCCFPCMAEFGSDENDASACTKCPNDPWSN 600
QY 601 ENHTSCIAKEIEVLSWTEPFGALITFAVLGILITSVFLGVPIKFNTPPIVKATNRELSY 660
DB 601 ENHTSCIAKEIEVLSWTEPFGALITFAVLGILITSVFLGVPIKFNTPPIVKATNRELSY 660
QY 661 LLLFSLICFSSSLIFIGSPDWTCLRPAPAFISFVLCISCIILVKNRVLVFEAKIPT 720
DB 661 LLLFSLICFSSSLIFIGSPDWTCLRPAPAFISFVLCISCIILVKNRVLVFEAKIPT 720
QY 721 SLHRKWWGNLQFLVFLCILVQIVTCIIWLVTAPSSYRNHELEDEVIPTCDGSLMA 780
DB 721 SLHRKWWGNLQFLVFLCILVQIVTCIIWLVTAPSSYRNHELEDEVIPTCDGSLMA 780
QY 781 LGFLIGYTCLLAACFFFAKSKRLPENFNEAKFITFSMLPIFFIWMISIPAYVSTYGF 840

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DB 781 LGFLIGYTCLLAACFFFAKSKRLPENFNEAKFITFSMLPIFFIWMISIPAYVSTYGF 840
QY 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCNTIEEVRCTAAHAFKVAARATLRS 900
DB 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCNTIEEVRCTAAHAFKVAARATLRS 900
QY 901 AASKRSSSLCGSTISSPASSTCGPGLTMEMQRCSTQKVSFGSGTTLTSLSEETGYAT 960
DB 901 AASKRSSSLCGSTISSPASSTCGPGLTMEMQRCSTQKVSFGSGTTLTSLSEETGYAT 960
QY 961 LSRTARSNSADGRSGDDLPSRHHQDPPQKCEFPQANDARYKAAPTKGTLESFGGSKER 1020
DB 961 LSRTARSNSADGRSGDDLPSRHHQDPPQKCEFPQANDARYKAAPTKGTLESFGGSKER 1020
QY 1021 PTTMEET 1027
DB 1021 PTTMEET 1027

RESULT 5
US-10-016-496-2
; Sequence 2, Application US/10016496
; Publication No. US20030166908A1
; GENERAL INFORMATION:
; APPLICANT: H. William Harris
; APPLICANT: Edward M. Brown
; APPLICANT: Steven C. Hebert
; TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
; FILE REFERENCE: 2856.1001-007
; CURRENT APPLICATION NUMBER: US/10/016,496
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US/09/162,021B
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: PCT/US97/05031
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 08/622,738
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: squalus acanthias
US-10-016-496-2

Query Match      100.0%; Score 5410; DB 14; Length 1027;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKDQDLKSRE 60
DB 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKDQDLKSRE 60
QY 61 ATKCIYRNFRGFWLQAMFAIEEINNMTFLPNITLGYRIEDTCTNTVSKALEATLSFVA 120
DB 61 ATKCIYRNFRGFWLQAMFAIEEINNMTFLPNITLGYRIEDTCTNTVSKALEATLSFVA 120
QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYPOVSYASSRLLSN 180
DB 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYPOVSYASSRLLSN 180
QY 181 KNEYKAFPLTIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRPGIDKFEAEVKRDI 240
DB 181 KNEYKAFPLTIPNDEQOATAMAEIIEHFQWNVGTLLAADDYGRPGIDKFEAEVKRDI 240
QY 241 IDPSEMISQYTKQLEFIADVIQNSAKVIVVFNNGDPLELIQEIIVRNITDRIWLAS 300
DB 241 IDPSEMISQYTKQLEFIADVIQNSAKVIVVFNNGDPLELIQEIIVRNITDRIWLAS 300
QY 301 EAWASSLLAKPEYFHVVGTTGFAIRAGRIEFGNKFKEVHPSRSSDNGFVKFEWETP 360

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Db 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPGFNFKFLKEVHPSSDNGFVKFWEETF 360  
Qy 361 NCYFTEKTLTQLNKSKVPSHGPAAGDGSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420  
Db 361 NCYFTEKTLTQLNKSKVPSHGPAAGDGSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420  
Qy 421 HLRIYNVAVYSIAHALQDIHSCPKPTGIFANGSCADIKKVEAWQVNLHLHLKFTNS 480  
Db 421 HLRIYNVAVYSIAHALQDIHSCPKPTGIFANGSCADIKKVEAWQVNLHLHLKFTNS 480  
Qy 481 MGEQVDFDDQGLKGNYYTIINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILMSG 540  
Db 481 MGEQVDFDDQGLKGNYYTIINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILMSG 540  
Qy 541 FSKVVPFNSCSDCVPGTRKGIIIEGPTCCFECMACAEGFSDENDASACTKCPNDFWSN 600  
Db 541 FSKVVPFNSCSDCVPGTRKGIIIEGPTCCFECMACAEGFSDENDASACTKCPNDFWSN 600  
Qy 601 ENHTSCIAKEIEYLSWTEPFGIALTIIPAVLGILITSFVLGVPIKFRNTPIVKATNRELSY 660  
Db 601 ENHTSCIAKEIEYLSWTEPFGIALTIIPAVLGILITSFVLGVPIKFRNTPIVKATNRELSY 660  
Qy 661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLICISCIILVKTNRVLLVFEAKIPT 720  
Db 661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLICISCIILVKTNRVLLVFEAKIPT 720  
Qy 721 SLHRKWGLNLQFLVFLCIVQITCIIWLVTAPSSVYNHELEDEVIFITCDEGSLMA 780  
Db 721 SLHRKWGLNLQFLVFLCIVQITCIIWLVTAPSSVYNHELEDEVIFITCDEGSLMA 780  
Qy 781 LGFLIGYTCLLAAICFFFAFKSKLPENFNEAKITFSMLIFFIWMISFIPAYVSTYCKF 840  
Db 781 LGFLIGYTCLLAAICFFFAFKSKLPENFNEAKITFSMLIFFIWMISFIPAYVSTYCKF 840  
Qy 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSAAHAFKVAARATLRRS 900  
Db 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSAAHAFKVAARATLRRS 900  
Qy 901 AASRKRSSLCGSTISSPASSTCGPLTMEMORCSTQKVSFGSGVTIILSLSFEETGRYAT 960  
Db 901 AASRKRSSLCGSTISSPASSTCGPLTMEMORCSTQKVSFGSGVTIILSLSFEETGRYAT 960  
Qy 961 LSRTARSNSADGRSGDDLPSSHHQCGPPQKCEPOPANDARYKAAPTKGTLESPOGSKER 1020  
Db 961 LSRTARSNSADGRSGDDLPSSHHQCGPPQKCEPOPANDARYKAAPTKGTLESPOGSKER 1020  
Qy 1021 PTTMEET 1027  
Db 1021 PTTMEET 1027

## RESULT 6

US-10-410-885-2  
; Sequence 2, Application US/10410885  
; Publication No. US2003023266A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, H. William  
; APPLICANT: Nearing, Jacqueline A.  
; APPLICANT: Betka, Marlies  
; TITLE OF INVENTION: Polyvalent Cation-Sensing Receptor in Atlantic Salmon  
; FILE REFERENCE: 2213,1006-008  
; CURRENT APPLICATION NUMBER: US/10/410,885  
; PRIORITY FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: 10/125,778  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: 10/125,772  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: 10/125,792  
; PRIOR FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: 10/121,441  
; PRIOR FILING DATE: 2002-04-11  
; PRIOR APPLICATION NUMBER: PCT/US01/31704  
; PRIOR FILING DATE: 2001-10-11

; PRIOR APPLICATION NUMBER: 60/240,392  
; PRIOR FILING DATE: 2000-10-12  
; PRIOR APPLICATION NUMBER: 60/240,003  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 1027  
; TYPE: PRT  
; ORGANISM: Squalus acanthias  
; US-10-410-885-2

Query Match 100.0%; Score 5410; DB 14; Length 1027;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1027; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MAQLHCOLLFLGTTLLQSYNVSGYGNQRAQKGDIIILGGLFPIHFGVAAKQDOLKS RPE 60  
Db 1 MAQLHCOLLFLGTTLLQSYNVSGYGNQRAQKGDIIILGGLFPIHFGVAAKQDOLKS RPE 60  
Qy 61 ATKIRYNFSGFRWLQAMIFAEIENNSMTFLFNITLGYRIFDTCTNTVSKALEATILSFVA 120  
Db 61 ATKIRYNFSGFRWLQAMIFAEIENNSMTFLFNITLGYRIFDTCTNTVSKALEATILSFVA 120  
Qy 121 QNKIDSNLNDEFNCSDHIPSTIAVVGATSGGISTAVANLLGLFYIPOVSYASSRLLSN 180  
Db 121 QNKIDSNLNDEFNCSDHIPSTIAVVGATSGGISTAVANLLGLFYIPOVSYASSRLLSN 180  
Qy 181 KNEYKAFIRIPINDEQOATAMABIIIEHFQNNWVGTAAADDYGRPGIDKFEAEAVKEDIC 240  
Db 181 KNEYKAFIRIPINDEQOATAMABIIIEHFQNNWVGTAAADDYGRPGIDKFEAEAVKEDIC 240  
Qy 241 IDFSEMIQYTTQKLEFFIADVIQNSAKVIVVFSNGPDLEPIQIEIVRENIITDRIWLAS 300  
Db 241 IDFSEMIQYTTQKLEFFIADVIQNSAKVIVVFSNGPDLEPIQIEIVRENIITDRIWLAS 300  
Qy 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPGFNFKFLKEVHPSSDNGFVKFWEETF 360  
Db 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPGFNFKFLKEVHPSSDNGFVKFWEETF 360  
Qy 361 NCYFTEKTLTQLNKSKVPSHGPAAGDGSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420  
Db 361 NCYFTEKTLTQLNKSKVPSHGPAAGDGSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420  
Qy 421 HLRIYNVAVYSIAHALQDIHSCPKPTGIFANGSCADIKKVEAWQVNLHLHLKFTNS 480  
Db 421 HLRIYNVAVYSIAHALQDIHSCPKPTGIFANGSCADIKKVEAWQVNLHLHLKFTNS 480  
Qy 481 MGEQVDFDDQGLKGNYYTIINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILMSG 540  
Db 481 MGEQVDFDDQGLKGNYYTIINWOLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKKILMSG 540  
Qy 541 FSKVVPFNSCSDCVPGTRKGIIIEGPTCCFECMACAEGFSDENDASACTKCPNDFWSN 600  
Db 541 FSKVVPFNSCSDCVPGTRKGIIIEGPTCCFECMACAEGFSDENDASACTKCPNDFWSN 600  
Qy 601 ENHTSCIAKEIEYLSWTEPFGIALTIIPAVLGILITSFVLGVPIKFRNTPIVKATNRELSY 660  
Db 601 ENHTSCIAKEIEYLSWTEPFGIALTIIPAVLGILITSFVLGVPIKFRNTPIVKATNRELSY 660  
Qy 661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLICISCIILVKTNRVLLVFEAKIPT 720  
Db 661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLICISCIILVKTNRVLLVFEAKIPT 720  
Qy 721 SLHRKWGLNLQFLVFLCIVQITCIIWLVTAPSSVYNHELEDEVIFITCDEGSLMA 780  
Db 721 SLHRKWGLNLQFLVFLCIVQITCIIWLVTAPSSVYNHELEDEVIFITCDEGSLMA 780  
Qy 781 LGFLIGYTCLLAAICFFFAFKSKLPENFNEAKITFSMLIFFIWMISFIPAYVSTYCKF 840  
Db 781 LGFLIGYTCLLAAICFFFAFKSKLPENFNEAKITFSMLIFFIWMISFIPAYVSTYCKF 840  
Qy 841 VSAVEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSAAHAFKVAARATLRRS 900

Db 841 VSAVEVIAIASSFGLGCIYFNKCVIIILFKCRNTIEEVRCTAAHAFKVAARATLRS 900  
 QY 901 AASRKSSSLCGSTISSPASSTCGPGLTWEMORCSTQKVSFGSGVTLSLSPFEETGRVAT 960  
 Db 901 AASRKSSSLCGSTISSPASSTCGPGLTWEMORCSTQKVSFGSGVTLSLSPFEETGRVAT 960  
 QY 961 LSTARSNSADRSDDLPSSRHDDGPPQKCEPOPANDARYKAAPTGTLESPOGSKER 1020  
 Db 961 LSTARSNSADRSDDLPSSRHDDGPPQKCEPOPANDARYKAAPTGTLESPOGSKER 1020  
 QY 1021 PTTMEET 1027  
 Db 1021 PTTMEET 1027  
 RESULT 7  
 US-09-727-205-2  
 ; Sequence 2, Application US/09727205  
 ; Patent No. US2002064813A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ELLIS, CATHERINE E.  
 ; TITLE OF INVENTION: MONKEY CALCIUM SENSING RECEPTOR  
 ; FILE REFERENCE: GP-70665  
 ; CURRENT APPLICATION NUMBER: US/09/727, 205  
 ; CURRENT FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: 60/168, 342  
 ; PRIOR FILING DATE: 1999-12-01  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1078  
 ; TYPE: PRT  
 ; ORGANISM: MACACA CYNOMOLGUS  
 US-09-727-205-2  
 Query Match 75.0%; Score 4055.5; DB 9; Length 1078;  
 Best Local Similarity 74.3%; Pred. No. 4.2e-307; Indels 51; Gaps 7;  
 Matches 785; Conservative 85; Mismatches 136;

QY 1 MAQLHCQLLFLGFTLLQSYNVSQYGNPQRAQKGGDIILGGLFPIHFGVAAKQDQLKS RPE 60  
 Db 1 MAFYCCFWLLALT---WHTSAYGPDQRAQKGGDIILGGLFPIHFGVAAKQDQLKS RPE 56  
 QY 61 ATKCYRNPGRFWLQAMIFAEIEINNSMTFLPNTLGYRIPTDTCNTVSKALEATLSFVA 120  
 Db 57 SVECIYRNPGRFWLQAMIFAEIEINNSMTFLPNTLGYRIPTDTCNTVSKALEATLSFVA 116  
 QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLGLFYIPQVSVASSRLLSN 180  
 Db 117 QNKIDSLNDEFNCSEHIPTIAVVGATGSGVSTAVANLGLFYIPQVSVASSRLLSN 176  
 QY 181 KNEYKAFRTIPNDQOATAMAEIEIHFQWNVVGTAAADDDYGRPGIDKFREEAVKRDIC 240  
 Db 177 KXQFKSFLTIPNDEHQATAMADIEYFRWNVVGTAAADDDYGRPGIEKFREEAEERDIC 236  
 QY 241 IDPSEMISOYTKOLEFTADVIONSSAKVIVVFSNGPDLEPLICEIVERNITDRIWLAS 300  
 Db 237 IDPSELISQISDEEIQHVIVQNSTAKVIVVFSNGPDLEPLICEIVERNITKILWAS 296  
 QY 301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIPGNKFLKEVHPSSSDNGFVKFEWETP 360  
 Db 297 EAWASSSLIAMPEYFHVVGTTIGFALKAQIPGFRFLKKVHPKRSVHNGFAKFEWETP 356  
 QY 361 NCYFTEKTIJQLKNSKVPESHGAAQDQSGSKANSRRTALRHPCTGEENITSVETPYLDYT 420  
 Db 357 NCHLOEGAKGPL---PVDFTLGHESGGRFNS--STAFRLCTGDNISVETPYDIYT 412  
 QY 421 HLRIISNVVAVYSIAHALQDIHSCPGTIGIFANGSCADIKKVEAQVNLHLHLKFTNS 480  
 Db 413 HLRIISNVVAVYSIAHALQDIYTCLPGRGLFTNGSCADIKKVEAQVNLHLHLFTNN 472  
 QY 481 MGEQVDFDQDGLKGNYYTINWQLSNAEDSVLFHEVGNVAYAKPSDRNLINNEKILLWSG 540

Db 473 MGEQVDFDECDLVGNYSIINWHLSPEDGSIKVPKEVYNNVYAKGERLFINEKILLWSG 532  
 QY 541 FSKVVPFNSCRVCVGTGRKGIIEGPTCCFECMACAEGEFSDENDASACTKCPDNFWSN 600  
 Db 533 FSREVPFNSCRDCLAGTRKGIIEGPTCCFECVCEPDGEYSDETASACNCKPDDFWSN 592  
 QY 601 ENHTSCIATKIEIYLSWTEPFGIALTIFAVLGILITISFVLGVIKFRNTPIVKATNRELSY 660  
 Db 593 ENHTSCIATKIEIYLSWTEPFGIALTIFAVLGILITISFVLGVIKFRNTPIVKATNRELSY 652  
 QY 661 LLLFSLICCFSSSLIFIGEPDWTCLROPAPGISFVLICISILVNTNRVLLVFEAKIPT 720  
 Db 653 LLLFSLICCFSSSLIFIGEPDWTCLROPAPGISFVLICISILVNTNRVLLVFEAKIPT 712  
 QY 721 SLHRKVVGLNLOQLLVFLCIIVOITCIWLVTAPPSSYRNHELEDEVIPTCDEGSLMA 780  
 Db 713 SPHRKWGLNLOQLLVFLCIIVOITCIWLVTAPPSSYRNHELEDEVIPTCDEGSLMA 772  
 QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFPIVWISFIPAVSYTGKP 840  
 Db 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITFSMLIFPIVWISFIPAVSYTGKP 832  
 QY 841 VSAVEVIAIASSFGLGCIYFNKCVIIILFKCRNTIEEVRCTAAHAFKVAARATLRS 900  
 Db 833 VSAVEVIAIASSFGLGCIYFNKCVIIILFKCRNTIEEVRCTAAHAFKVAARATLRS 892  
 QY 901 AASRKSSSLCGSTISSPASSTCGPG-----DTMEM 931  
 Db 893 NVSRKSSSLGGSTGTSTPSSISSKNSBDPPPERKQKQPPALTOEQEQOQPLTLQ 952  
 QY 932 Q-----RCSTQKVSFGSGVTLSLSPFEETGRVATLSATARSNSADRSDDLPSSRH 984  
 Db 953 QQQSQQQPRCK-QKVIFFSGTIVTSLSFDEPQKNAVAHENSTHQSLEAKQSSDTLARH- 1010  
 QY 985 DQGPQKCEPOPANDARYKAAPTGTLESFGGSKERP 1021  
 Db 1011 -----QALLPQCEADSLSVQETGLQGVGDHRP 1042  
 RESULT 8  
 US-10-159-339-8  
 ; Sequence 8, Application US/10159339  
 ; Publication No. US20030166540A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,  
 ; FILE REFERENCE: D0169NP  
 ; CURRENT APPLICATION NUMBER: US/10/159,339  
 ; CURRENT FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: US 60/294,411  
 ; PRIOR FILING DATE: 2001-05-30  
 ; NUMBER OF SEQ ID NOS: 94  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 8  
 ; LENGTH: 1078  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-159-339-8  
 Query Match 74.8%; Score 4044.5; DB 14; Length 1078;  
 Best Local Similarity 74.0%; Pred. No. 3e-306;  
 Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;

QY 1 MAQLHCQLLFLGFTLLQSYNVSQYGNPQRAQKGGDIILGGLFPIHFGVAAKQDQLKS RPE 60  
 Db 1 MAFYCCFWLLALT---WHTSAYGPDQRAQKGGDIILGGLFPIHFGVAAKQDQLKS RPE 56  
 QY 61 ATKCYRNPGRFWLQAMIFAEIEINNSMTFLPNTLGYRIPTDTCNTVSKALEATLSFVA 120  
 Db 57 SVECIYRNPGRFWLQAMIFAEIEINNSMTFLPNTLGYRIPTDTCNTVSKALEATLSFVA 116



841 VSAVEVIAILASSFGLGCIYNNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900  
 833 VSAVEVIAILASSFGLGCIYNNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 892  
 901 AASRKSSSLGSGTSSPASS\*CGPG-----LTWEM 931  
 893 NVSRKRSSSLGSGTSSPASS\*CGPG-----LTWEM 931  
 932 Q-----RCSTQKVSFGSGTTLTSLSPFETGYATLSTARSNSADGRGDDLPSSHH 984  
 953 QRSQQPRCK-QKVFSGTGTFTSLSPFETGYATLSTARSNSADGRGDDLPSSHH 1010  
 985 DOGPPQKCEPQANDARYKAAPTGTLSPPGSGKERP 1021  
 1011 -----QPLFLQCGGTDLDLTVOETGLQGPVGGDQRP 1042

RESULT 10  
 US-10-436-715-74  
 ; Sequence 74, Application US/10436715  
 ; Publication No. US20040018976A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,  
 ; AND SPLICE VARIANTS THEREOF  
 ; FILE REFERENCE: D0262 NP  
 ; CURRENT APPLICATION NUMBER: US/10/436,715  
 ; PRIOR FILING DATE: 2003-05-13  
 ; PRIOR APPLICATION NUMBER: U.S. 60/380,336  
 ; NUMBER OF SEQ ID NOS: 471  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 74  
 ; LENGTH: 1078  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-436-715-74

Query Match 74.8%; Score 4044.5; DB 15; Length 1078;  
 Best Local Similarity 74.0%; Pred. No. 3e-306;  
 Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;

1 MAQLHCOLLFLGFTLLQSYNVSGYGNORAKKGGIILGGLFPIHFGVAAKQDQLKSRE 60  
 1 MAFYSCCWLLALT-----WHTSAYGPDQRAKKGDIILGGLFPIHFGVAAKQDQLKSRE 56  
 61 ATKCIYRNFRGFWLQAMIFATEEINNSMTLPNTLTGVRIFDTCNTVSKALEATLSFA 120  
 57 SVEICIRYNFRGFWLQAMIFATEEINNSMTLPNTLTGVRIFDTCNTVSKALEATLSFA 116  
 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPQVYASSRLLSN 180  
 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPQVYASSRLLSN 176  
 181 KNEYKAFRTINDECOATAMEIIEHQWVWGLAADDYGRGIDKPEEAKVRDIC 240  
 177 KNOFKSFLRTINDESHQATAMADIIEYFRWVWGLAADDYGRGIDKPEEAKVRDIC 236  
 241 IDPSEMISQYTKOLEFIADYQNSAKVIIVFVSGNGDPLELQIEIVRNITRIMLAS 300  
 237 IDPSELISQYSDBEIHHQVVEIQNSTAKVIIVFVSGNGDPLELQIEIVRNITRIMLAS 296  
 301 EAWASSLIATAPEYHVVGGTIGFALRAGRIPGKFKFKEVHPSRSSDNGFKFWEETP 360  
 297 EAWASSLIATAPEYHVVGGTIGFALRAGRIPGKFKFKEVHPSRSSDNGFKFWEETP 356  
 361 NCVFETKTUTQKNSVPVSHGPAACDGSKAGNSRRTALRHPCTGEENITSVEPYLDYT 420  
 357 NCHLQEGAKGPL---PVDTFLEHESGDRFNS--STAFRLCTGDNISSEVPIIDYT 412  
 421 HLRIISYNYVAVYSIAHALODIHSCKPGTGFANGSCADIKKVEAQVNLHLHKKFTNS 480  
 413 HLRIISYNYVAVYSIAHALODIHSCKPGTGFANGSCADIKKVEAQVNLHLHKKFTNS 472

481 MGQVDPDDQGLKNGYTIINWOLSAEDSVLPHEVGNVYNAKPSDRNLNINEKKILMSG 540  
 473 MGQVDPDDQGLKNGYTIINWOLSAEDSVLPHEVGNVYNAKPSDRNLNINEKKILMSG 532  
 541 FSKVVPFNSCRDVCPTGRKGIIEGPTCCFECMACAECEGFEFSDENDASACTKCPNDFWSN 600  
 533 FSEVFNSCRDVCPTGRKGIIEGPTCCFECMACAECEGFEFSDENDASACTKCPNDFWSN 592  
 601 ENHTSCIAKEIEYLSWTEPFGIALTIPAVLIGLITSLFVLGVFIKFRNTPIVKAATRELSY 660  
 593 ENHTSCIAKEIEYLSWTEPFGIALTIPAVLIGLITSLFVLGVFIKFRNTPIVKAATRELSY 652  
 661 LLLFSLICCFSSSLIFIGEPDWTCLROPAGISFVLGICILVKTNRVLLVFEAKIPT 720  
 653 LLLFSLICCFSSSLIFIGEPDWTCLROPAGISFVLGICILVKTNRVLLVFEAKIPT 712  
 721 SLHRKVMGLNLQFLVFLCIVLQIVTCTIILWLTAPSSSYRNHELEDEVIFITCDEGLMA 780  
 713 SPHRKVMGLNLQFLVFLCIVLQIVTCTIILWLTAPSSSYRNHELEDEVIFITCDEGLMA 772  
 781 LGFLIGYTCLLAAICFFFAFKSRKLPENENAKFITFSMLIFELIWIISFIPAVVSYGKF 840  
 773 LGFLIGYTCLLAAICFFFAFKSRKLPENENAKFITFSMLIFELIWIISFIPAVVSYGKF 832  
 841 VSAVEVIAILASSFGLGCIYNNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900  
 833 VSAVEVIAILASSFGLGCIYNNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 892  
 901 AASRKSSSLGSGTSSPASS\*CGPG-----LTWEM 931  
 893 NVSRKRSSSLGSGTSSPASS\*CGPG-----LTWEM 931  
 932 Q-----RCSTQKVSFGSGTTLTSLSPFETGYATLSTARSNSADGRGDDLPSSHH 984  
 953 QRSQQPRCK-QKVFSGTGTFTSLSPFETGYATLSTARSNSADGRGDDLPSSHH 1010  
 985 DOGPPQKCEPQANDARYKAAPTGTLSPPGSGKERP 1021  
 1011 -----QPLFLQCGGTDLDLTVOETGLQGPVGGDQRP 1042

Query Match 74.8%; Score 4044.5; DB 15; Length 1078;  
 Best Local Similarity 74.0%; Pred. No. 3e-306;  
 Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;

1 MAQLHCOLLFLGFTLLQSYNVSGYGNORAKKGGIILGGLFPIHFGVAAKQDQLKSRE 60  
 1 MAFYSCCWLLALT-----WHTSAYGPDQRAKKGDIILGGLFPIHFGVAAKQDQLKSRE 56  
 61 ATKCIYRNFRGFWLQAMIFATEEINNSMTLPNTLTGVRIFDTCNTVSKALEATLSFA 120

```

Db 57 SVECIYRFRGRFWLQAMIFAIEEINSSPALLNLTLGYRIPDTCTNTVSKALEATLSFVA 116
QY 121 QNKIDSLNLDPCNCSDDHPSSTIAVVGATGSGISTAVANLLGLFYIPOVSVASSRLLSN 180
Db 117 QNKIDSLNLDPCNCSDDHPSSTIAVVGATGSGISTAVANLLGLFYIPOVSVASSRLLSN 176
QY 181 KNEYKAFURITPNDQOQATAMAEIIIEHFQWNVWGTAAADDDYGRPGIDKPREAVKRDIC 240
Db 177 QNKQKSLRITPNDQOQATAMAEIIIEHFQWNVWGTAAADDDYGRPGIEKPREAEERDIC 236
QY 241 IDSEMIQYITCKOLEFIADVIQNSAKVIVFSGDPLBPLQEIIVRNITDRILWAS 300
Db 237 IDFSLLISQYSDDEEIQHVVEIQNSTAKVIVFSSGPDLEPLKIEIVRNITKILWAS 296
QY 301 EAWASSLSIAKPEYHVHVGTTIGFALRAGRIPGFNFKLKEVHPKSSDNGFVKFWBEET 360
Db 297 EAWASSLSIAMPQYHVHVGTTIGFALRAGIPGFNFKLKEVHPKSVHNGFAKEFWBEET 356
QY 361 NCYFTEKTLTQLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGEBNITSVETPYLDYT 420
Db 357 NCHLQEGAKGPL--PVDTFLRGHEESGDRFNS--STAFRPLCTGDNISVETPYLDYT 412
QY 421 HLRISYNNVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAWQVNLHLLKFTNS 480
Db 413 HLRISYNNVAVYSIAHALQDIYTCLPORGFTNGSCADIKKVEAWQVNLHRLNFTNN 472
QY 481 MGEQVDFDDQDGLKONYTIIINWQSAEDSVLFHEVGNYNAYAKPSDRNLNEXKILWSG 540
Db 473 MGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGNVYAKKGERLFINEEKILWSG 532
QY 541 FSKVVPFNSCRDVCYGRKGIIEGPTCCPECMAEGBESDENDASACTKCPNDFWSN 600
Db 533 FSREVFPNSCRDCLAGRKGIIEGPTCCPECVCEPDGGEYSDETDASACNKPDDFWSN 592
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSVLGFVKPRNTPIVKATNRELSY 660
Db 593 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSVLGFVKPRNTPIVKATNRELSY 652
QY 661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLICISILVKTNRVLLVFEAKIPT 720
Db 653 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLICISILVKTNRVLLVFEAKIPT 712
QY 721 SLHRKWGLNLQFLVFLCIIQVITCIWLTAPSSYRNHELEDEVIITCDEGSLMA 780
Db 713 SLHRKWGLNLQFLVFLCIIQVITCIWLTAPSSYRNHELEDEVIITCDEGSLMA 772
QY 781 LGFLIGYTCIIAAICFFFAFKSRKLPENFNFAKFTTSMILFFIIVISFIPAYVSTYKGF 840
Db 773 LGFLIGYTCIIAAICFFFAFKSRKLPENFNFAKFTTSMILFFIIVISFIPAYVSTYKGF 832
QY 841 VSAVEVIAIASSFGLGCIYFNKCYIILFKPCNTIIEVRCSTAAHAFKVAARATLRS 900
Db 833 VSAVEVIAIASSFGLGCIYFNKCYIILFKPCNTIIEVRCSTAAHAFKVAARATLRS 892
QY 901 AASRRKSSLCGSTISSPASSTCGPG-----LTWEM 931
Db 893 NVSRKSSSLGGSTGSTSSSISSKSNSEDPFPQPERKQOQPLALTOEQOQQPLTLQP 952
QY 932 Q-----RCSTQKVSFGSVITLSLFEETGRVATLSRTARSNSADGRSGDLLPSRHH 984
Db 953 QQRQSQOQPRCK-QKVFISGVTLSLFEDEPQKNAMAHNSHTQNSLEAQKSSDTLTRH- 1010
QY 985 DQGPQKCEPOPANDARYKAAPTKGTLESPPGSKERP 1021
Db 1011 -----QPLLPLOCGTDLTLVQETGLOGVGGDQRP 1042

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RESULT 12

```

US-10-408-765A-171
; Sequence 171, Application US/10408765A
; Publication No. US200401018741
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Scumitra S.

```

```

; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408, 765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171
; LENGTH: 1078
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-171

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Query Match 74.8%; Score 4044.5; DB 16; Length 1078;
Best Local Similarity 74.0%; Pred. No. 3e-306;
Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;

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QY 1 MAQLHCOLLFLGFTLLQSNVSCYGNORAKKGDIIILGLRPFIFHFGVAAKQDCLSRPE 60
Db 1 MAYSCCWLALUT---WHTSAYQDQRAKKGDIIILGLRPFIFHFGVAAKQDCLSRPE 56
QY 61 ATKIRYNFRGFRWLQAMIFAIEEINSSMTFLPNITLGYRIPDTCTNTVSKALEATLSFVA 120
Db 57 SVECIYRFRGRFWLQAMIFAIEEINSSPALLNLTLGYRIPDTCTNTVSKALEATLSFVA 116
QY 121 QNKIDSLNLDPCNCSDDHPSSTIAVVGATGSGISTAVANLLGLFYIPOVSVASSRLLSN 180
Db 117 QNKIDSLNLDPCNCSDDHPSSTIAVVGATGSGISTAVANLLGLFYIPOVSVASSRLLSN 176
QY 181 KNEYKAFURITPNDQOQATAMAEIIIEHFQWNVWGTAAADDDYGRPGIDKPREAVKRDIC 240
Db 177 QNKQKSLRITPNDQOQATAMAEIIIEHFQWNVWGTAAADDDYGRPGIEKPREAEERDIC 236
QY 241 IDSEMIQYITCKOLEFIADVIQNSAKVIVFSGDPLBPLQEIIVRNITDRILWAS 300
Db 237 IDFSLLISQYSDDEEIQHVVEIQNSTAKVIVFSSGPDLEPLKIEIVRNITKILWAS 296
QY 301 EAWASSLSIAKPEYHVHVGTTIGFALRAGRIPGFNFKLKEVHPKSSDNGFVKFWBEET 360
Db 297 EAWASSLSIAMPQYHVHVGTTIGFALRAGIPGFNFKLKEVHPKSVHNGFAKEFWBEET 356
QY 361 NCYFTEKTLTQLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGEBNITSVETPYLDYT 420
Db 357 NCHLQEGAKGPL--PVDTFLRGHEESGDRFNS--STAFRPLCTGDNISVETPYLDYT 412
QY 421 HLRISYNNVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAWQVNLHLLKFTNS 480
Db 413 HLRISYNNVAVYSIAHALQDIYTCLPORGFTNGSCADIKKVEAWQVNLHRLNFTNN 472
QY 481 MGEQVDFDDQDGLKONYTIIINWQSAEDSVLFHEVGNYNAYAKPSDRNLNEXKILWSG 540
Db 473 MGEQVTFDECGDLVGNYSIINWHLSPEDGSIVFKEVGNVYAKKGERLFINEEKILWSG 532
QY 541 FSKVVPFNSCRDVCYGRKGIIEGPTCCPECMAEGBESDENDASACTKCPNDFWSN 600
Db 533 FSREVFPNSCRDCLAGRKGIIEGPTCCPECVCEPDGGEYSDETDASACNKPDDFWSN 592
QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSVLGFVKPRNTPIVKATNRELSY 660
Db 593 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGILITSVLGFVKPRNTPIVKATNRELSY 652
QY 661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLICISILVKTNRVLLVFEAKIPT 720
Db 653 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLICISILVKTNRVLLVFEAKIPT 712
QY 721 SLHRKWGLNLQFLVFLCIIQVITCIWLTAPSSYRNHELEDEVIITCDEGSLMA 780

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Db 713 SPHRKRWGLNQLFLVFLCTFMQIVICWLVYADPPSYRNQELDEIIFITCHEGSLMA 772  
 QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITPMSLFFIIVWISFIPAYVSTYKGF 840  
 Db 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITPMSLFFIIVWISFIPAYVSTYKGF 832  
 QY 841 VSAVEVIAILASFGLLGCIYKNCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRS 900  
 Db 833 VSAVEVIAILASFGLLGCIYKNCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRS 892  
 QY 901 AASRRKSSSLGSGTSSPASSCTGPG-----LTWEM 931  
 Db 893 NVSRKSSSLGSGTSSPASSCTGPG-----LTWEM 952  
 QY 932 Q-----RCSTOKVSFGSGTTLTSLSFETGRYATLSTARSNSADGRSGDLPSPHH 984  
 Db 953 QORSQQPRCK-QKVFSGSGTTFSLSFDEPKQNAHNSHTQNSLEAKSSDTLTRH- 1010  
 QY 985 DQGPQKCEPQANDARYKAATKGTLESPPGSKERP 1021  
 Db 1011 -----QPLLPQCGETDLDLTVOETGLQGVGGDQRP 1042

RESULT 13  
 US-10-002-854-2  
 ; Sequence 2, Application US/10002854  
 ; Publication No. US20020132224A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Scadden, David T.  
 ; APPLICANT: Pozhansky, Mark C.  
 ; APPLICANT: Olszak, Ivona T.  
 ; APPLICANT: Brown, Edward M.  
 ; TITLE OF INVENTION: THE CAR RECEPTOR AS A MEDIATOR OF  
 ; MIGRATORY CELL CHEMOATAXIS AND/OR CHEMOKINESIS  
 ; FILE REFERENCE: M0765/7038/ERG/KA  
 ; CURRENT APPLICATION NUMBER: US/10/002,854  
 ; CURRENT FILING DATE: 2001-11-01  
 ; PRIOR APPLICATION NUMBER: PCT/US00/15440  
 ; PRIOR FILING DATE: 2000-06-02  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 1078  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)...(1078)  
 ; OTHER INFORMATION: Ca-sensing Receptor  
 US-10-002-854-2

Query Match 74.7%; Score 4039.5; DB 13; Length 1078;  
 Best Local Similarity 73.9%; Pred. No. 7.4e-306;  
 Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

QY 1 MAQLHCQLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAQDQDKSRPE 60  
 Db 1 MAFYSCWVLLALT-----WHTSAYGPDQRAQKGGDIILGGLFPIHFGVAQDQDKSRPE 56  
 QY 61 ANKCIYRFRGRWLQAMVFAIEENNSMTFLPNTITLGYRFDTCNTVSKALEATLSFVA 120  
 Db 57 SVECIYRFRGRWLQAMVFAIEENNSMTFLPNTITLGYRFDTCNTVSKALEATLSFVA 116  
 QY 121 QNKIDSLNLFDFCNSDHTPSTIAVVGATGSGISTAVANLGLFYIPQSVASSRLLSN 180  
 Db 117 QNKIDSLNLFDFCNSDHTPSTIAVVGATGSGISTAVANLGLFYIPQSVASSRLLSN 176  
 QY 181 KNEYKAFRTIPNDEQOATAMAEIIEHFCWNVGTLAADDYGRPGIDKPREEAVKRDIC 240  
 Db 177 KNOFSFLRTIPNDEHQAAMADIIIEYFRWNVGTLAADDYGRPGIEKPREEAEERDIC 236  
 QY 241 IDPSEMISQYTKQLEFIADYQNSAKVIVVFGSGPDLEPLIQEIVERNITPRILWAS 300

Db 237 IDESELIQSDEEBEIQHVVEVIQNSTAKVIVVFGSGPDLEPLIKEIVERNITGKIWLAS 296  
 QY 301 EAWASSSLIAKPEYFHVVGTTGTFALRAGRIIPGNKFLKEVHPSSSDNGFVKBEWEETF 360  
 Db 297 EAWASSSLIAKPEYFHVVGTTGTFALRAGRIIPGNKFLKEVHPSSSDNGFVKBEWEETF 356  
 QY 361 NCYFTEKTLTQKNKSPVSHGPAQDGSKAGNSRRTALRHPTGBENITTSVETPYLDYT 420  
 Db 357 NCHLQGAKGPL---PDTFLRGHEESGDRFNS-STARPLCTGDNISSEVETPYDIT 412  
 QY 421 HLRISNVYVAVYSIAHALQDIHSCKPGTGIIFANGSCADIKKVEAWQVNLHLHLKFTNS 480  
 Db 413 HLRISNVYVAVYSIAHALQDIHSCKPGTGIIFANGSCADIKKVEAWQVNLHLHLNFTNN 472  
 QY 481 MGEQVDFDQGDILKGNITINWLSAEDSVLPHEVGNYNAYAKPSDRNLNINEKILWSG 540  
 Db 473 MGEQVDFDQGDILKGNITINWLSAEDSVLPHEVGNYNAYAKPSDRNLNINEKILWSG 532  
 QY 541 FSKVVPFNSCRDVCPTGRKGIIEGPTCCFCMACAEGEFSDENDASACTCPNDPWSN 600  
 Db 533 FSREVPFNSCRDVCPTGRKGIIEGPTCCFCMACAEGEFSDENDASACTCPNDPWSN 592  
 QY 601 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGLILITSLFVLGVFIKFRNTPIVATNRELSY 660  
 Db 593 ENHTSCIAKEIEYLSWTEPFGIALTIFAVLGLILITSLFVLGVFIKFRNTPIVATNRELSY 652  
 QY 661 LLLFSLICCFSSSLIFIGEPDWTCLROPATGIFSVLCISILVKTNRVLLVFEAKIPT 720  
 Db 653 LLLFSLICCFSSSLIFIGEPDWTCLROPATGIFSVLCISILVKTNRVLLVFEAKIPT 712  
 QY 721 SLHRKWGLNQLFLVFLCTFMQIVICWLVYADPPSYRNQELDEIIFITCHEGSLMA 772  
 Db 713 SPHRKRWGLNQLFLVFLCTFMQIVICWLVYADPPSYRNQELDEIIFITCHEGSLMA 772  
 QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITPMSLFFIIVWISFIPAYVSTYKGF 840  
 Db 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFITPMSLFFIIVWISFIPAYVSTYKGF 832  
 QY 841 VSAVEVIAILASFGLLGCIYKNCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRS 900  
 Db 833 VSAVEVIAILASFGLLGCIYKNCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRS 892  
 QY 901 AASRRKSSSLGSGTSSPASSCTGPG-----LTWEM 931  
 Db 893 NVSRKSSSLGSGTSSPASSCTGPG-----LTWEM 952  
 QY 932 Q-----RCSTOKVSFGSGTTLTSLSFETGRYATLSTARSNSADGRSGDLPSPHH 984  
 Db 953 QORSQQPRCK-QKVFSGSGTTFSLSFDEPKQNAHNSHTQNSLEAKSSDTLTRH- 1010  
 QY 985 DQGPQKCEPQANDARYKAATKGTLESPPGSKERP 1021  
 Db 1011 -----QPLLPQCGETDLDLTVOETGLQGVGGDQRP 1042

RESULT 14  
 US-10-225-567A-118  
 ; Sequence 118, Application US/10225567A  
 ; Publication No. US20030113798A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LifeSpan Biosciences  
 ; APPLICANT: Brown, Joseph P.  
 ; APPLICANT: Barner, Glenna C.  
 ; TITLE OF INVENTION: ANTIGENIC L.  
 ; FILE REFERENCE: 1920-4-4  
 ; CURRENT APPLICATION NUMBER: US/10/225,567A  
 ; CURRENT FILING DATE: 2001-12-19  
 ; PRIOR APPLICATION NUMBER: 60/257,144  
 ; PRIOR FILING DATE: 2000-12-19  
 ; NUMBER OF SEQ ID NOS: 2292  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 118



Qy 932 Q-----RCSTQKVGSGTSLTSLSFETGRYATLSRTARSRNADGRSGDDLPSSRH 984  
Db 953 QQRSSQOPRCK-QKVIKSGTSLTSLSFDEPQKNAHNGSTHONSLEAKSSDITLTH- 1010  
Qy 985 DQPPPKCBPQANDARYKAAPTGTGLESPPGSKERP 1021  
Db 1011 -----QPLLPLQCGTDLDTVOETGLQGPVGQDRP 1042

RESULT 15  
US-10-673-888-1  
; Sequence 1, Application US/10673889  
; Publication No. US20040082588A1  
; GENERAL INFORMATION:  
; APPLICANT: Evans, Ellen  
; APPLICANT: Choy, Wai Nang  
; APPLICANT: Mario, Elmer  
; TITLE OF INVENTION: METHODS FOR TREATING DISORDERS OF CALCIUM HOMEOSTASIS  
; FILE REFERENCE: OC01600-US  
; CURRENT APPLICATION NUMBER: US/10/673,889  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: 60/414,948  
; PRIOR FILING DATE: 2002-09-30  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 1088  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (537)..(546)  
; OTHER INFORMATION: deleted in human calcium ion sensing receptor variant  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (936)..(936)  
; OTHER INFORMATION: Q in human calcium ion sensing receptor variant  
; NAME/KEY: VARIANT  
; LOCATION: (1000)..(1000)  
; OTHER INFORMATION: G in human calcium ion sensing receptor variant  
US-10-673-888-1

Query Match 74.5%; Score 4029.5; DB 15; Length 1088;  
Best Local Similarity 73.3%; Pred. No. 4.5e-305;  
Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;

Qy 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKQDQLSRPE 60  
Db 1 MAFVSCCWLALT-----WHTSAYGPDQRAQKGGDIILGGLFPIHFGVAAKQDQLSRPE 56,  
Qy 61 ATKIRYNFRGFRWLQAMIFAEIEINNSMTFLNITLGYRIPTCTNTVSKALEATLSFVA 120  
Db 57 SVEICIRYNFRGFRWLQAMIFAEIEINNSPALLFNLTGLYRIPTCTNTVSKALEATLSFVA 116  
Qy 121 QNKIDSLNLDNFCNCSHPSTIAVVGATGSGTAVANLLGLFYIPOVSYASSSRLSN 180  
Db 117 QNKIDSLNLDNFCNCSHPSTIAVVGATGSGTAVANLLGLFYIPOVSYASSSRLSN 176  
Qy 181 KNEYKAPLRTIPNDEQOATAMAEIIEHFQNNWVGTLAADDYGRPGIDKPREBAVRDIC 240  
Db 177 KNQPKSLRTIPNDEHQATAMADIIEYFRNNWVGTLAADDYGRPGIEKFEBAERDIC 236  
Qy 241 IDSEMSISQYTKOLEFIADIVQNSAKVIVVFSNGPDLLEPLIOEIVRNITDRIWLAS 300  
Db 237 IDSEMSISQYDEEEQHVVEVIONSTAKVIVVFSNGPDLLEPLIOEIVRNITDRIWLAS 296  
Qy 301 EAWASSSLIAKPYFHVVGTTIGFALRAGRIPGKFKLEVHPSRSDNGFVKFEWETF 360  
Db 297 EAWASSSLIAMPQYFHVVGTTIGFALKAGQIPGFRFLKKVHPRKSVHNGFAKEWETF 356  
Qy 361 NCYFTEKTLTQLKNSKVPKSHGPAQGGSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420  
Db 357 NCHLQEGAGPL--PVDIFLGRHEESGDRPNS-STAFRLCTGDNISSVETPYDIT 412  
Qy 421 HLRISYVTVAVYSTAHALQDTHSKPGTGTFANGSCADIKKVEAWQVNLHLHLKFTNS 480  
Db 413 HLRISYVTVAVYSTAHALQDITCLPGRGLFTNGSCADIKKVEAWQVNLHLHLNFTNN 472  
Qy 481 MGEQVDFDQGLKNGYTIINWOLSAEDSVLFHEVGNVNAVAKDPSRLNINEKKILWSG 540  
Db 473 MGEQVTFECGLDVGNSYIINWHLSPEDGSIIVKGVYNNYAKGERLFINEEKILWSG 532  
Qy 541 FSKVYFNCSDCVGTRKGIIEGPTCCFCMACAEGFSDENDASACTKCPNDFWSN 600  
Db 533 FSRVYFNCSDCLAGTRKGIIEGPTCCFCVCEPCDGEYSDENDASACNKCPCDDFSN 592  
Qy 601 ENHTSCIAKEIYLSKTBPGTALTIPAVLGYLTITSFVLGVYFIERNTPIVKATNRELSY 660  
Db 593 ENHTSCIAKEIBFLSWTBPGTALTIPAVLGYLTITSFVLGVYFIERNTPIVKATNRELSY 652  
Qy 661 LLLFSLICFSSSLIFIGEPDRWTCRLRQPAFGISFVLICISILVKNRVLVFEAKIPT 720  
Db 653 LLLFSLICFSSSLIFIGEPDQWTCRLRQPAFGISFVLICISILVKNRVLVFEAKIPT 712  
Qy 721 SLHRKVGUNLQFLVFLCILVQIVTCIWLITAPSSYRNHELEDEVIFITCEGSLMA 780  
Db 713 SPHRKVGUNLQFLVFLCFTQIVICVWLITAPSSYRNQOELEDEVIFITCEGSLMA 772  
Qy 781 LGFLGYTCLLAAICFFFAFKSRKLPENENEAFTFSMLIFFIWMISFIPAYVSTYKGF 840  
Db 773 LGFLGYTCLLAAICFFFAFKSRKLPENENEAFTFSMLIFFIWMISFIPAYVSTYKGF 832  
Qy 841 VSAVEVIALASFGLLGCYINKYIILFKPCRNITBEVRCSTAAHAFKVAARATLRS 900  
Db 833 VSAVEVIALAASFGLLACIFENKIYIILFKPSRNTIBEVRCSTAAHAFKVAARATLRS 892  
Qy 901 AASRKSLSLGGSTISSPASSCGPG-----LTWEM 931  
Db 893 NVSRKRSLSLGGSTGSPSSISKSNSDDPPFPQERKQOPLALTOEQOQQLTLPQ 952

Qy 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAAKQDQLSRPE 60  
Db 1 MAFVSCCWLALT-----WHTSAYGPDQRAQKGGDIILGGLFPIHFGVAAKQDQLSRPE 56  
Qy 61 ATKIRYNFRGFRWLQAMIFAEIEINNSMTFLNITLGYRIPTCTNTVSKALEATLSFVA 120  
Db 57 SVEICIRYNFRGFRWLQAMIFAEIEINNSPALLFNLTGLYRIPTCTNTVSKALEATLSFVA 116  
Qy 121 QNKIDSLNLDNFCNCSHPSTIAVVGATGSGTAVANLLGLFYIPOVSYASSSRLSN 180  
Db 117 QNKIDSLNLDNFCNCSHPSTIAVVGATGSGTAVANLLGLFYIPOVSYASSSRLSN 176  
Qy 181 KNEYKAPLRTIPNDEQOATAMAEIIEHFQNNWVGTLAADDYGRPGIDKPREBAVRDIC 240  
Db 177 KNQPKSLRTIPNDEHQATAMADIIEYFRNNWVGTLAADDYGRPGIEKFEBAERDIC 236  
Qy 241 IDSEMSISQYTKOLEFIADIVQNSAKVIVVFSNGPDLLEPLIOEIVRNITDRIWLAS 300  
Db 237 IDSEMSISQYDEEEQHVVEVIONSTAKVIVVFSNGPDLLEPLIOEIVRNITDRIWLAS 296  
Qy 301 EAWASSSLIAKPYFHVVGTTIGFALRAGRIPGKFKLEVHPSRSDNGFVKFEWETF 360  
Db 297 EAWASSSLIAMPQYFHVVGTTIGFALKAGQIPGFRFLKKVHPRKSVHNGFAKEWETF 356  
Qy 361 NCYFTEKTLTQLKNSKVPKSHGPAQGGSKAGNSRRTALRHPCTGTEENITSVETPYLDYT 420  
Db 357 NCHLQEGAGPL--PVDIFLGRHEESGDRPNS-STAFRLCTGDNISSVETPYDIT 412  
Qy 421 HLRISYVTVAVYSTAHALQDTHSKPGTGTFANGSCADIKKVEAWQVNLHLHLKFTNS 480  
Db 413 HLRISYVTVAVYSTAHALQDITCLPGRGLFTNGSCADIKKVEAWQVNLHLHLNFTNN 472  
Qy 481 MGEQVDFDQGLKNGYTIINWOLSAEDSVLFHEVGNVNAVAKDPSRLNINEKKILWSG 540  
Db 473 MGEQVTFECGLDVGNSYIINWHLSPEDGSIIVKGVYNNYAKGERLFINEEKILWSG 532  
Qy 541 FSKVYFNCSDCVGTRKGIIEGPTCCFCMACAEGFSDENDASACTKCPNDFWSN 600  
Db 533 FSRVYFNCSDCLAGTRKGIIEGPTCCFCVCEPCDGEYSDENDASACNKCPCDDFSN 592  
Qy 601 ENHTSCIAKEIYLSKTBPGTALTIPAVLGYLTITSFVLGVYFIERNTPIVKATNRELSY 660  
Db 593 ENHTSCIAKEIBFLSWTBPGTALTIPAVLGYLTITSFVLGVYFIERNTPIVKATNRELSY 652  
Qy 661 LLLFSLICFSSSLIFIGEPDRWTCRLRQPAFGISFVLICISILVKNRVLVFEAKIPT 720  
Db 653 LLLFSLICFSSSLIFIGEPDQWTCRLRQPAFGISFVLICISILVKNRVLVFEAKIPT 712  
Qy 721 SLHRKVGUNLQFLVFLCILVQIVTCIWLITAPSSYRNHELEDEVIFITCEGSLMA 780  
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Qy 781 LGFLGYTCLLAAICFFFAFKSRKLPENENEAFTFSMLIFFIWMISFIPAYVSTYKGF 840  
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Qy 841 VSAVEVIALASFGLLGCYINKYIILFKPCRNITBEVRCSTAAHAFKVAARATLRS 900  
Db 833 VSAVEVIALAASFGLLACIFENKIYIILFKPSRNTIBEVRCSTAAHAFKVAARATLRS 892  
Qy 901 AASRKSLSLGGSTISSPASSCGPG-----LTWEM 931  
Db 893 NVSRKRSLSLGGSTGSPSSISKSNSDDPPFPQERKQOPLALTOEQOQQLTLPQ 952

Db 357 NCHLQBGAKGPL---PVDTFLECHESGDRFSNS-STAFRLCTGDENISSVETPYIDYT 412  
QY 421 HLRISTNVYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAQVNLHLHKLFTNS 480  
Db 413 HLRISTNVYVAVYSIAHALQDIYVCLPGRLFTNGSCADIKKVEAQVNLHLHKLFTNN 472  
QY 481 MGEQVDFDQDGLKGNYYIINQLSAEDSVLFHEVGNVYAKPSDRNLNINEKILWSG 540  
Db 473 MGEQVTFDECGDLVGNYSIINHLSPEDGSIYVKEVGYNVYAKGERLFINEEKILWSG 532  
QY 541 FSK-----VVPFSCSRDCVPGTRKGIIEGPTCCPECMACARGEFSDENDASAC 590  
Db 533 FPREPLTFVLSVLQVFFNCSRDCLAGTRKGIIEGPTCCPECVCPDGEYSDETDASAC 592  
QY 591 TKCPDNDFWSENHTSCIAKEIYLSWTEPPFGIALTIFAVLGILITSFVLGVFIKFRNTPI 650  
Db 593 NKCPDDFWSENHTSCIAKEIEFLSWTEPPFGIALTFAVLGIFLFAVLGVFIKFRNTPI 652  
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Db 653 VKATNRELSYLLFSLICCFSSSLFIFGEPODWTCLRQPAFGISFVLCISCLLVKTNV 712  
QY 711 LNVFEAKIPTSLHRKWVGNLQFLVFLCILVOIVTCIWLVTAPPSSYRNHELEDEVIP 770  
Db 713 LNVFEAKIPTSPHRKWVGNLQFLVFLCTFMQIVICVWLVTAPPSSYRNQELEDEIIF 772  
QY 771 ITCDEGSLMALGLIGYTCLLAAICFFFAFKSRKLPENFNEAKPITFSMLIFFIWIISFI 830  
Db 773 ITCHEGSLMALGLIGYTCLLAAICFFFAFKSRKLPENFNEAKPITFSMLIFFIWIISFI 832  
QY 831 PAYVSTYKGFVSAREVIAIALASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFK 890  
Db 833 PAYVSTYKGFVSAREVIAIALASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFK 892  
QY 891 VAARATLRSASRSKSSSLCGSTISSPASSTCGPG----- 926  
Db 893 VAARATLRSNSVRSKSSSLGSGTGSTPSSISSKSNSBEDPFRPERKQOQPLALTOQE 952  
QY 927 -----LTMEMQ-----RCSTQKVSFGSGTVTLISLFEETGRYATLSRTARSNSADGR 974  
Db 953 QOQOPLTLPOQORSQOQFCK-QKVFSGTVTFSLSPDEPKAMAHNSTHONSLEAQ 1011  
QY 975 SGDDLPSRHHQGPQKCEPQANDARYKAAPTGTLESPPGSKERP 1021  
Db 1012 KSSDTLTRH-----QPLPLQCGETDLDLTVOETGLQGPVGGDQRP 1052

Search completed: November 17, 2004, 12:37:31  
Job time : 520 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 17, 2004, 11:02:39 ; Search time 73 Seconds  
(without alignments)

1353.625 Million cell updates/sec

Title: US-10-016-496-2

Perfect score: 5410

Sequence: 1 MAQHCOLLFLGFTLLQSYN.....KGTLESPGSGSKERPTTMEET 1027

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4037.5	74.6	1078	2 A56715	calcium receptor (
2	4029.5	74.5	1088	2 B56715	calcium receptor (
3	3998.5	73.9	1085	2 S40476	Ca(2+)-sensing rec
4	3996	73.9	1079	2 I59362	calcium/polyvalent
5	1145	21.2	879	2 JH0562	metabotropic gluta
6	1137	21.0	879	2 JC7160	metabotropic gluta
7	1115.5	20.6	912	2 JH0563	metabotropic gluta
8	1114.5	20.6	872	2 JH0561	metabotropic gluta
9	1108.5	20.5	871	2 A46742	metabotropic gluta
10	1092.5	20.2	915	2 A49874	metabotropic gluta
11	1077	19.9	908	2 I49142	metabotropic gluta
12	1056.5	19.5	1212	2 JC2131	metabotropic gluta
13	1052	19.4	1199	2 A41939	G protein-coupled
14	1044	19.3	1171	2 A42916	metabotropic gluta
15	1040	19.2	1180	2 JC2132	metabotropic gluta
16	1017.5	18.8	858	2 JC7683	taste receptor T1R
17	1015.5	18.8	1218	2 S71376	glutamate receptor
18	1005.5	18.6	999	2 T27628	hypothetical prote
19	888	16.4	1267	2 T21340	hypothetical prote
20	682	12.6	1551	2 T30806	metabotropic gluta
21	365	6.7	1099	2 T16283	hypothetical prote
22	216	4.0	921	2 T51136	ionotropic glutama
23	215	4.0	923	2 F84732	probable ligand-ga
24	210.5	3.9	953	2 E84732	probable ligand-ga
25	206	3.8	997	2 S33754	glutamate receptor
26	205	3.8	951	2 T51132	probable glutamate
27	203	3.8	950	2 T51134	ionotropic glutama
28	201	3.7	925	2 T51133	ligand gated chann
29	199	3.7	965	2 I51244	N-methyl-D-asparta

#### RESULT 1

A56715

calcium receptor (clone pncAR-4.0) - human

C/Species: Homo sapiens (man)

C/Date: 19-Oct-1995 #sequence revision 19-Oct-1995 #text\_change 01-Dec-2000

C/Accession: A56715; S49341; A49419; B49419; C49419

R/Garratt J.E.; Capuano I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.

J. Biol. Chem. 270, 12319-12925, 1995

A/Title: Molecular cloning and functional expression of human parathyroid calcium receptor

A/Reference number: A56715; MUID:95279439; PMID:7759551

A/Accession: A56715

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1078 <GAR>

A/Cross-references: GB:020759; NID:G683744; PIDN:AAA6503.1; PID:G683745

R/Pearce, S.H.S.; Thakker, R.V.

submitted to the EMBL Data Library, August 1994

A/Reference number: S49341

A/Accession: S49341

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-180, 'Q', 182-989, 'R', 991-1078 <PEA>

A/Cross-references: EMBL:X81086

R/Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi, J.

Cell 75, 1297-1303, 1993

A/Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalcemic

A/Reference number: A49419; MUID:94094324; PMID:7515660

A/Accession: A49419

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 178-192 <POL>

A/Experimental source: family N

A/Note: sequence inconsistent with nucleotide translation

A/Note: sequence modified after extraction from NCBI backbone

A/Note: 186-Arg mutation is associated with familial hypocalcemic hypercalcemia and neor

A/Accession: B49419

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 289-303 <PO2>

A/Experimental source: family E

A/Note: sequence modified after extraction from NCBI backbone

A/Note: 298-Lys mutation is associated with familial hypocalcemic hypercalcemia and neor

A/Accession: C49419

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 788-802 <PO3>

A/Experimental source: family J

A/Note: sequence modified after extraction from NCBI backbone

A/Note: 796-Trp mutation is associated with familial hypocalcemic hypercalcemia and neor

A/Accession: A56715

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 788-802 <PO3>

A/Experimental source: family J

A/Note: sequence modified after extraction from NCBI backbone

A/Note: 796-Trp mutation is associated with familial hypocalcemic hypercalcemia and neor

A/Accession: A56715

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 788-802 <PO3>

A/Experimental source: family J

A/Note: sequence modified after extraction from NCBI backbone

A/Note: 796-Trp mutation is associated with familial hypocalcemic hypercalcemia and neor

C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 74.6%; Score 4037.5; DB 2; Length 1078;  
Best Local Similarity 73.3%; Pred. No. 2.8e-287;  
Matches 781; Conservative 86; Mismatches 139; Indels 51; Gaps 7;

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DB 1 MAFYSCWVLLALT----WHTSAYGPDQRAQKKGDIILGGLPPIHFGVAAKQDQLKSRE 56
QY 61 ATKIRYNFRGRFWLQAMIFALIEEINNSMTFIPNITLGYRIEDTCTNTVSKALEATLSFVA 120
DB 57 SVEICIRYNFRGRFWLQAMIFALIEEINNSMTFIPNITLGYRIEDTCTNTVSKALEATLSFVA 116
QY 121 QNKIDSLNLDLFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180
DB 117 QNKIDSLNLDLFCNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 176
QY 181 KNEYKAFRTIPNDEQOATAMAEIIEHFQWNVGTLLAADDDYGRGIDKFRFEAVKRDIC 240
DB 177 KNQFKSFLRTIPNDEHQATAMADIIEYFRWNVGTLLAADDDYGRGIDKFRFEAEERDIC 236
QY 241 IDPSEMISOYVTKOLEFTADVIQNSAKVIVVFSNGPDLEPLIQEIVRRNITDRIWLAS 300
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QY 301 EAWASSSLIAKPEYFHVVGTTGFALRAGRIPOFNKFLKEVHPSSSDNGFVKFEWEETP 360
DB 297 EAWASSSLIAMPQYFHVVGTTGFALRAGRIPOFNKFLKEVHPSSSDNGFVKFEWEETP 356
QY 361 NCYFTEKTLTQLKNSKVPESHGPAAGDQSGKAGNSRRTALRHPCTGSENIITSVETPYLDYT 420
DB 357 NCHLQEGAKGPL---PVDTFLRGHESGDRFNS--STAFPRDCTGDNISVETPYIDYT 412
QY 421 HLRISYNYVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAQVNLHLHLKFTNS 480
DB 413 HLRISYNYVAVYSIAHALQDIYVCLPGRGLFTNGSCADIKKVEAQVNLHLHLFTNN 472
QY 481 MGEQVDFDQGDILKGYNTIINQLSNADESIVLFEVGNVYAKPSDRNLNINEKILLWSG 540
DB 473 MGEQVTFDCGDLVGNYSIINWHLSPEDGSIYVFEVGNVYAKGERLFINEEKILLWSG 532
QY 541 FSKVVPFNSCRDVPGRKGIIIEGPTCCFECMACAEFSDENDASACTKCPDNDFWSN 600
DB 533 FSRVFPFNSCRDCLAGTRKGIIEGPTCCFECVCPGECSDETDASACNKPDDFWSN 592
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DB 593 ENHTSCIAKEIYLSWTEPFGIALTIFAVLGILITTSFVLGVFKPRNTPIVKATNRELSY 652
QY 661 LLLFSLICCFSSSLFIPIGPRDWTCLRLQPAFGISFVLICISILVKNRLLVPEAKIPT 720
DB 653 LLLFSLICCFSSSLFIPIGEPQDWTCLRLQPAFGISFVLICISILVKNRLLVPEAKIPT 712
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DB 713 SFHRKVGUNLOFLVFLICILVOITCIIWLVTAPPSYRNHELEDEVFITCDEGSLMA 772
QY 781 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFTIPSLMIFFIWISFIPAYVSTYKGF 840
DB 773 LGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKFTIPSLMIFFIWISFIPAYVSTYKGF 832
QY 841 VSAVEVIALASSFGLGCIYFNKCYIILFKPCRNITIEEVRCSSTAHAHFKVAARATLRS 900
DB 833 VSAVEVIALAASFGLLACIFFNKCYIILFKPCRNITIEEVRCSSTAHAHFKVAARATLRS 892
QY 901 AASRRSSSLCGSTISSPASSTCGPG-----LTMEN 931
DB 893 NVSRKSSSLGSGTSTSPSSISSKNSBEDPPQPEROKQOQPLALTOOEOQOQPLTLFQ 952
QY 932 Q-----RCSTQKVSFGSGVTLSLSPETGRYATLSRTARSNSADGRSGDGLPSRHH 984
DB 953 QOESQOQPRCK-QKVIKFGSGTVPFSLSDPEPKNAWAGNSHQNSLEAKSSDTLTFH- 1010
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QY 985 DOGPPQKCEPQANDARYKAAPTGTLESPPGSKERP 1021  
DB 1011 -----QPLLFLQCGETDLDTVQETGLQGVGGDQRP 1042

## RESULT 2

B56715

calcium receptor (clone phrCar-5.2) - human

C;Species: Homo sapiens (man)

C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000

C;Accession: B56715

R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.C.

J. Biol. Chem. 270, 12919-12925, 1995

A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor

A;Reference number: A56715; MUID:95279439; PMID:7759551

A;Accession: B56715

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1088 &lt;GAR&gt;

A;Cross-references: GB:U02760; NID:G683746; PIDN:AAA86504.1; PID:G683747

C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 74.5%; Score 4029.5; DB 2; Length 1088;  
Best Local Similarity 73.3%; Pred. No. 1.1e-286;  
Matches 782; Conservative 86; Mismatches 138; Indels 61; Gaps 8;

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DB 1 MAFYSCWVLLALT----WHTSAYGPDQRAQKKGDIILGGLPPIHFGVAAKQDQLKSRE 56
QY 61 ATKIRYNFRGRFWLQAMIFALIEEINNSMTFIPNITLGYRIEDTCTNTVSKALEATLSFVA 120
DB 57 SVEICIRYNFRGRFWLQAMIFALIEEINNSMTFIPNITLGYRIEDTCTNTVSKALEATLSFVA 116
QY 121 QNKIDSLNLDLFCNCSDHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180
DB 117 QNKIDSLNLDLFCNCSEHIPSTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 176
QY 181 KNEYKAFRTIPNDEQOATAMAEIIEHFQWNVGTLLAADDDYGRGIDKFRFEAVKRDIC 240
DB 177 KNQFKSFLRTIPNDEHQATAMADIIEYFRWNVGTLLAADDDYGRGIDKFRFEAEERDIC 236
QY 241 IDPSEMISOYVTKOLEFTADVIQNSAKVIVVFSNGPDLEPLIQEIVRRNITDRIWLAS 300
DB 237 IDPSELISQYSDDEEIQHVVEVIQNSTAKVIVVFSNGPDLEPLIQEIVRRNITDRIWLAS 296
QY 301 EAWASSSLIAKPEYFHVVGTTGFALRAGRIPOFNKFLKEVHPSSSDNGFVKFEWEETP 360
DB 297 EAWASSSLIAMPQYFHVVGTTGFALRAGRIPOFNKFLKEVHPSSSDNGFVKFEWEETP 356
QY 361 NCYFTEKTLTQLKNSKVPESHGPAAGDQSGKAGNSRRTALRHPCTGSENIITSVETPYLDYT 420
DB 357 NCHLQEGAKGPL---PVDTFLRGHESGDRFNS--STAFPRDCTGDNISVETPYIDYT 412
QY 421 HLRISYNYVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAQVNLHLHLKFTNS 480
DB 413 HLRISYNYVAVYSIAHALQDIYVCLPGRGLFTNGSCADIKKVEAQVNLHLHLFTNN 472
QY 481 MGEQVDFDQGDILKGYNTIINQLSNADESIVLFEVGNVYAKPSDRNLNINEKILLWSG 540
DB 473 MGEQVTFDCGDLVGNYSIINWHLSPEDGSIYVFEVGNVYAKGERLFINEEKILLWSG 532
QY 541 FSKVVPFNSCRDVPGRKGIIIEGPTCCFECMACAEFSDENDASACTKCPDNDFWSN 590
DB 533 FSRVFPFNSCRDCLAGTRKGIIEGPTCCFECVCPGECSDETDASACNKPDDFWSN 592
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DB 593 NKCPDDFWSNENHTSCIAKEIYLSWTEPFGIALTIFAVLGILITTSFVLGVFKPRNTP 652
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Db	773	ITCHEGSMALGFLIGYTCLLAACIFFAFPKSRKLPENFNEAKFTTFMSLFFIWIWSFI	832
Qy	831	PAYVSTYGFVSAAVEVIAIALASSFGLLGCITYENKNKVIIILFKPCRNTEIEEVRCS	890
Db	833	PAYASTYGFVSAAVEVIAIALASSFGLLGCITYENKNKVIIILFKPCRNTEIEEVRCS	892
Qy	891	VAARATLRSAASRRKSSSLCGSTISSPASSTCGPG-----	926
Db	893	VAARATLRSNVSRKSSSLGGSTGSTPSSSSSKSNSDDPPFRPEROKQQQLALTQOE	952
Qy	927	-----LTMEMQ-----RCSTQKVSFGSGTTVLSLSPETGRYATLSTRARSNSADGR	974
Db	953	QOQOPLTLPOQRSQOPRCK-QKVIFGSGTTVFSLSDFPKPMAWHNSTHQNSLEAQ	1011
Qy	975	SGDDLFSRHHDQPPQKCBFPANDARYKAAPTGTLESFGSGSKRP	1021
Db	1012	KSSDTLTRH-----QPLLPLQGGETDLTLTQETGLQGVGDQRP	1052
Db	RESULT 3		
Qy	S40476	Ca(2+)-sensing receptor - bovine C:Species: Bos primigenius taurus (cattle) C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 C:Accession: S40476 R:Brown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifer, O.; Sun, A.; H Nature 366, 575-580, 1993 A:Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from B A:Reference number: S40476; MUID:94077182; PMID:8255296 A:Accession: S40476 A>Status: preliminary A:Molecule type: mRNA A:Residues: 1-1085 <BRO> A:Cross-references: UNIPROT:P35384; GB:S67307; NID:G453108; PIDN:AAB29171.1; PID:G453109	
Query Match	73.9%	Score 3999.5;	DB 2; Length 1085;
Best Local Similarity	72.8%	Pred. No. 1.7e-284;	
Matches	778;	Conservative 92;	Mismatches 141; Indels 57; Gaps 8;
Qy	1	MAQLHCQLFLGLTLLQSYNVSGYNORQAQKGDIILGLRLPIHFGVAQKDQLKSRE	60
Db	1	MALYSQCWILLAFS---TWTSAYGDPQRAQKGDIIILGLRPIHFGVAQKDQLKSRE	57
Qy	61	ATKCIRYNFRGFWLQAMIFAIBEINNMSTFLENITLGYRIPTCNTVSKALEATLSFVA	120
Db	58	SVCEIRYNFRGFWLQAMIFAIBEINSSPALLENMTLGYRIPTCNTVSKALEATLSFVA	117
Qy	121	QNKIDSUNLDFCNCSHIPTTAVNGATSGISTAVANLLGLFYTPQVSYASSSELSEN	180
Db	118	QNKIDSUNLDFCNCSHIPTTAVNGATSGISTAVANLLGLFYTPQVSYASSSELSEN	177
Qy	181	KNEYKAPLRTPNDEQQTAMATIEHFQNNWVGTLAADDYGRPGIDKFREAEVRKDC	240
Db	178	KNQFKSLRTPNDEHQATMADIIEYFRWNWVGTLAADDYGRPGIEFREAEERDC	237
Qy	241	IDSEMITSOYTKOLEFIADVTONSAAKVIUVFSGPDLEPLIQIIVERNITDRWLAS	300
Db	238	IDFELISIOYSDEKIQQVVEVTQNSTAKVIUVFSSGPDLLEPLIKEIVRNITGRWLAS	297
Qy	301	EAWASSLLIAKPEYFHVVGGTIGFALRAGRIPGNFKLVHPHSRSNDNGFVKFEWEETF	360
Db	298	EAWASSLLIAKPEYFHVVGGTIGFGLKAGQIPGREFLOKHPRKSHVNGFAKEFWEEIF	357
Qy	361	NCYTEKTTLQLKNSKVPSPHGPAQDGSGKAGNSRRRTALRHPTCGENTITSUTPYLDYT	420
Db			
Db	358	NCHLQEGAKGPL---PVDTFLRCHGEGBGARLNS-PTAFRPLCTGEBENISSVETPMWDYT	413
Qy	421	HLRISYNYVAVYSIAHALQDIHSCXPGTGFI FANGSCADIKKVKAQVNLHLLHLKFTNS	480
Db	414	HLRISYNYVAVYSIAHALQDIYTCIPGRGLFTNGSCADIKKVKAQVNLHLLHLNFTSN	473
Qy	481	MGQVDFDOGDGLKGNVTYTIINWOLSAEDSVLWFHEVGNYNAYAKPSDRLINIKKILWSG	540
Db	474	MGQVTFDECDLAGNYSIINWHLSPEDGSIVFKEVGYNYVYAKKERLFINDEKILWSG	533
Qy	541	FSKWPFNSCRDVCVPTRGKIIIEGECTCCPECMACAEGEFSDENDASACTKCPDNDFSN	600
Db	534	FSREVFPNSCRDCLAGRKIIIEGECTCCFECVECPDGEYSDETDASACDKCPDDFWSN	593
Qy	601	ENHTSCIAXEIEVLSWTEPGIALTIPAVLGILITSFVLGVFKPFRNTIIVKATNRELST	660
Db	594	ENHTSCIAXEIEFELSWEPPGIALTIPAVLGILITAFVLGVFKPFRNTIIVKATNRELST	653
Qy	661	LLLFSLICCFSSSLIPIGEPRDWTCRLQPAFGISFVLCISCILVKTNRVLLVFEAKIPT	720
Db	654	LLLFSLLCCFSSSLFIIGEPODWTCLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPT	713
Qy	721	SLHRKWGLNLQFLVLCILVQIVTCIWLTYAPPSYRNHELEDEVIFITCDEGSLMA	780
Db	714	SFHRKWGLNLQFLVLCITFMQIVICAIWNTAPPSSYRNHELEDEIIFITCHEGSLMA	773
Qy	781	LGFLLIGYTCLLAAACIFFAFPKSRKLPENFNEAKFTTFMSLFFIWIWSFI PAYVSTYGKF	840
Db	774	LGFLLIGYTCLLAAACIFFAFPKSRKLPENFNEAKFTTFMSLFFIWIWSFI PAYVSTYGKF	833
Qy	841	VSAVEVIAIALASSFGLLGCITYFNKCVIIILFKPCRNTEIEEVRCSAAHAFKVAARATLR	900
Db	834	VSAVEVIAIALASSFGLLGCITYFNKCVIIILFKPSRNTIEEVRCSAAHAFKVAARATLR	893
Qy	901	AASKRSSSLCGSTISSPASSTCG-----	925
Db	894	NVSRQRSLSLGGSTGSTPSSSISSKNSDEPFPQQQPKRQKQPQLALSHPNAQQQPRP	953
Qy	926	GLTNEMQ-----RCSTQKVSFGSGTVTLSPLETGRYATLSTRARSNSADGSGDD	978
Db	954	PSTPQPPQSQQPPRCK-QKVIFGSGTTVFSLSDFPKPMAWHNSTHQTSLEAQKND	1012
Qy	979	LPSRHHDQPPQKCEPQANDARYKAAPTGTLESFGSGSKERTTTEE	1026
Db	1013	ALTRH-----QALLPQCGTSETLSTQSTGTGQPVG-EDHQLEMED	1053
Db	RESULT 4		
Qy	159362	calcium/polyvalent cation-sensing receptor precursor - rat C:Species: Rattus norvegicus (Norway rat) C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 C:Accession: I59362; A55594 R:Ruut, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H. Proc. Natl. Acad. Sci. U.S.A. 92, 3161-3165, 1995 A:Title: Calcium sensing receptor: molecular cloning in rat and localization to nerve te A:Reference number: I59362; MUID:95241465; PMID:7724534 A:Accession: I59362 A>Status: translated from GB/EMBL/DDBJ A:Molecule type: mRNA A:Residues: 1-1079 <RES> A:Cross-references: UNIPROT:P48442; EMBL:U20289; NID:G790578; PIDN:AACS2195.1; PID:G790578 A:Experimental source: striatal R:Riccardi, D.; Park, J.; Lee, W.S.; Gamba, G.; Brown, E.M.; Hebert, S.C. Proc. Natl. Acad. Sci. U.S.A. 92, 131-135, 1995 A:Title: Cloning and functional expression of a rat kidney extracellular calcium/polyval A:Reference number: A55594; MUID:95116508; PMID:7816802 A:Accession: A55594 A:Molecule type: mRNA A:Residues: 1-133, 'X', 135-1079 <RIC> A:Cross-references: GB:U10354 A:Experimental source: kidney C:Keywords: calcium; glycoprotein; phosphoprotein; transmem	

F;1-20/Domain: signal sequence #status predicted <SIG>

F;187-212/Region: hydrophobic  
F;613-635/Domain: transmembrane #status predicted <TM1>  
F;650-670/Domain: transmembrane #status predicted <TM2>  
F;683-700/Domain: transmembrane #status predicted <TM3>  
F;725-744/Domain: transmembrane #status predicted <TM4>  
F;770-790/Domain: transmembrane #status predicted <TM5>  
F;806-828/Domain: transmembrane #status predicted <TM6>  
F;841-860/Domain: transmembrane #status predicted <TM7>  
F;90-261,287,386,468,488,594,893,1005/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;924/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F;899,901/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 73.9%; Score 3996; DB 2; Length 1079;  
Best Local Similarity 73.7%; Pred. No. 3,1e-284;  
Matches 780; Conservative 85; Mismatches 140; Indels 54; Gaps 8;

QY 1 MAQLHQLLFLGFTLLQSTNVSGYGNQRAQKGGDIILGGLPIHFGVAAKQDILKSRE 60  
DB 1 MASYSCLALLAL---AWHSSAYGPDQRAQKGGDIILGGLPIHFGVAAKQDILKSRE 56  
QY 61 ATKCIYRFRGFWLQAMIFAEIEINNSMTPLNTLGYRIFDTCTNTVSKALEATLSFVA 120  
DB 57 SVECIYRFRGFWLQAMIFAEIEINNSPSPLLPNWTLGYRIFDTCTNTVSKALEATLSFVA 116  
QY 121 QNKIDSLNDFPCNSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 180  
DB 117 QNKIDSLNDFPCNSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSVASSRLLSN 176  
QY 181 KNEYKAFRTIPNDEQATAMAEIIEHFQWNVGTAAADDDYGRGIDKFEAEAVKRDIC 240  
DB 177 KQYKSLFTIPNDEHQATAMAEIIEHFQWNVGTAAADDDYGRGIDKFEAEAEERDIC 236  
QY 241 IDPSEMISQYTKQLEFIADYVIONSSAKVIVVFSNGPDLEPLIOEIVRNRITRIWLAS 300  
DB 237 IDPSELISQYSDEEIQVVEIQNSAKVIVVFSNGPDLEPLIOEIVRNRITRIWLAS 296  
QY 301 EAWASSLLTAKPEYFHVVGCTGFALRAGRIIPGNKFLKEVHPSRSSNGFVKFEWETP 360  
DB 297 EAWASSLLTAKPEYFHVVGCTGFALRAGRIIPGNKFLKEVHPSRSSNGFVKFEWETP 356  
QY 361 NCYFEKTLTQLK-NSKVPDSHPAAQGGSGKAGNSRRRTALRHPCTGEENITSVETPYLDY 419  
DB 357 NCHLOEGAKGPLVDTFVRSH---EEGGNRLNS-STAFPLCTGDENINSVETPYMDY 411  
QY 420 THLRISYNYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVNLHLHLKFTN 479  
DB 412 EHLRISYNYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVNLHLHLKFTN 471  
QY 480 SMGEQVDFDDQGLKGNVYIINWQLSAEDSVLPFEVGNVYAYAKPSDRLNINEKILLWS 539  
DB 472 NMGEQVDFDECDLVGNYSIINWHLSPEDGSIVFEVGNVYAYAKPSDRLNINEKILLWS 531  
QY 540 GFSKVVPNSCRDCVPTGRKGIIEGPTCCFECMACAEGFSDENDASATKCPNDFWS 599  
DB 532 GFSREVFPNSCRDCVPTGRKGIIEGPTCCFECMACAEGFSDENDASATKCPNDFWS 591  
QY 600 NENHTSCIAKEIYLSWTEPFGLTIFAVLGILTTSFVLGVFIKFRNTPVKAATNELS 659  
DB 592 NENHTSCIAKEIYLSWTEPFGLTIFAVLGILTTSFVLGVFIKFRNTPVKAATNELS 651  
QY 660 YLLFSLICCFSSSLIFIGEPDWTCLRLQPAFGISFVLCISCLILKTNRLVLLFEAKIP 719  
DB 652 YLLFSLICCFSSSLIFIGEPDWTCLRLQPAFGISFVLCISCLILKTNRLVLLFEAKIP 711  
QY 720 TSLHKKWGLNQLFLLVFLCILVQITCIILWLTAPPSSYNNHELEDEVIITCEGLSM 779  
DB 712 TSFHRKRWGLNQLFLLVFLCILVQITCIILWLTAPPSSYNNHELEDEVIITCEGLSM 771  
QY 780 ALGFLIGYTCLLAAICFFFAFKSKLPENFNEAKPIFTSMLIFFIVWISFIPAVSYTYGK 839  
DB 772 ALGSLIGYTCLLAAICFFFAFKSKLPENFNEAKPIFTSMLIFFIVWISFIPAVSYTYGK 831

QY 840 FVSAREVIALASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRR 899  
DB 832 FVSAREVIALASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRR 891  
QY 900 SAASRKSSSLICGTSSTISSPASSTCGPG-----LTWE 930  
DB 892 PNISRKSSSLIGSGTSGIPSSSISSKNSRDRFPQPERKQOQPLSLTQOQQOPLTLH 951  
QY 931 MQ-----RCSTQKVSFGSGVTVLSLFEETGRVATLSRTARSNSADGRSGDDLPSR 982  
DB 952 PQOQQOQPRCK-QKVFISGVTFLSLSPDEPKNAHNRNSNRQNSLEAQRNSDTLGR 1010  
QY 983 HHDQGPQKCEPQFANDARYKAAFTKGTLESPPGSKERP 1021  
DB 1011 H-----QALLPLQCADSEMIIQETGLQGPVWGDHP 1043

RESULT 5  
JH0562  
metabotropic glutamate receptor 3 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: JH0562  
R:Tanabe, Y.; Masu, M.; Ishii, T.; Shigenoto, R.; Nakanishi, S.  
Neuron 8, 169-179, 1992  
A:Title: A family of metabotropic glutamate receptors.  
A:Reference number: JH0561; MUID:92110002; PMID:1309649  
A:Accession: JH0562  
A:Molecule type: mRNA  
A:Residues: 1-879 <TAN>  
A:Cross-references: UNIPROT:P31422  
A:Experimental source: brain  
C:Comment: This protein is coupled to a G protein and evokes a variety of functions by me  
C:Superfamily: metabotropic glutamate receptor 4  
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>  
F:577-599/Domain: transmembrane #status predicted <TM1>  
F:614-634/Domain: transmembrane #status predicted <TM2>  
F:646-664/Domain: transmembrane #status predicted <TM3>  
F:689-709/Domain: transmembrane #status predicted <TM4>  
F:735-756/Domain: transmembrane #status predicted <TM5>  
F:770-791/Domain: transmembrane #status predicted <TM6>  
F:804-828/Domain: transmembrane #status predicted <TM7>  
F:209,292,414,439/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:610,845/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 21.2%; Score 1145; DB 2; Length 879;  
Best Local Similarity 32.0%; Pred. No. 1.8e-75;  
Matches 306; Conservative 159; Mismatches 362; Indels 128; Gaps 33;

QY 7 QLFL-----GFTL-LQSYNVSGYGNQRAQKGGDIILGGLPIHFGVAAKQDILKSRE 60  
DB 8 QILMLALFKSGFTLSLGDHNF-----RREIKIEGDLVLGLGFLPN-----EKGTG 53  
QY 61 ATKCIYR-FRGRFWQAMIFAEIEINNSMTPLNTLGYRIFDTCTNTVSKALEATLSFV 119  
DB 54 TEECGRINEDRGRIQRLAEMLPAIDENKYNLLPGVGLGHILDTCSRDTYALEQSLEFV 113  
QY 120 --AQNKIDSLN---DEFNCSDHIPSTIA-VVGATGSGISTAVANLLGLFYIPQVSVAS 173  
DB 114 RASLTVDAAEYMCPPDGYSYAIQENIPLLIAGVIGSSYSVQVANLLRFLFOIPQISVAS 173  
QY 174 SSRLLSNKNEYKAFRTIPNDEQATAMAEIIEHFQWNVGTAAADDDYGRGIDKFEAE 233  
DB 174 TSAKSDSKRYDYFARTVPPDFYQAKMAEIRFFNWTYVTSVASEGDTGETGIEAFQEE 233  
QY 234 AVKRDICIDFSEMIQYTKQLE-FIADVIONSSAKVIVVFSNGPDLEPLIOEIVRNR 292  
DB 234 ARLRNICIAEAKVGRSNIRKSYDVSIRELLQKPNARVVLPMRSDSDRELIAAANRVN- 292  
QY 293 TDRWLASAWASSLLTAKPEYFHVVGCTGFALRAGRIIPGNKFLKEVHPSRSSNGFV 352



293 ASFTWASDGGWGAQESIVKGE-HVAYGAILTELASHPVRQFDYFQSLNPNHRRPWF 351  
 353 KEFWEETNCFVTEKTTTQLKNSKVPKSHGPAQGGKAGNSRRRTALRHPCTGEENTISV 412  
 352 RDFWEQKFC-----SLQNR-----NHRQVCDKHLAIDSSN--- 383  
 413 ETPVLDYTHLRISYNYVAVYSIAHALQDI-HSCKPGTGIFANGSCADIKKVEAWQVLN- 470  
 384 ---YEQESKIMFVN---AVYAMAHALHMKORTLCPTN-----TKLCDAMKILDG 427  
 471 -----HLLHLKFTNSMGEQ-----VDFDQDGLKNGYTIINWQLSAEDESULFHEVGN 518  
 428 KKLYKEYLLKINFAPFNPKNKAGSIVKFDFTFGDMGRYVNFNLQQTGGKYSYL--KVGH 485  
 519 YNAVAKSDRLNINEKKILWGFSGKVPFNSCRDVPGRKGIIEGEPCCRECMACAE 578  
 486 W-----AETLSLDVDSIHWGRNS--VPTSCSDPCAPNEMKNMQPGD-VCCWICICEP 536  
 579 GEFSDENDASACTKCPNDFWSENHTSCIAKEIEBLSWTEPFGIALTIFAVLGLITISV 638  
 537 YEYL--VDEFTCMDCGPGQWPTADLSGCYNLPEDYIKWEDAWAIGPVTIACGLFCLCIV 594  
 639 LGVFIKFNNTIVKATNRELSYLLFSLICFSSSLFIPGEPDWTCELQPAFGISFVL 698  
 595 ITVFIKHNTPLVKASGRELCCYLLFGVSLSYCMTEFFFIAPKSPVICALRLGLTGFAL 654  
 699 CISCILVNRVLLVFEAKIPTSLHRKQWVGLNLOPLLVFLC---ILVQIVTCIIWLYTAP 755  
 655 CYSALLTKTNCIARIFDGVKGAQPKFISPSQ---VFICLGLILVQIVWVSVLILET 711  
 756 PSSYRNHELED--EVIFITC---DEGSLMALGFLIGYTCLLAAICFFFAFKSRKLPENFN 810  
 712 PGT-RRYTLPEKRETVILKCNVKSMLISL---TYDWLVILCTVYAFKTRKCPENFN 766  
 811 BAKFTFSLMFFIWNISFIAYVSTYKGF--VSAVEVAILLAGSGLGCIYFNKCVII 868  
 767 BAKFTGFTYTTTCIIWLAFPIFYVTSDDYRVQITWTCISVLSGVFVGLCLFAPKXHV 826  
 869 LFKPCRNTIEEVRCSSTAHAFAKVAARATLRRSAASKRSSLG-----STISS 917  
 827 LFQPKQNVVTH---RLHLNRFVSCTATYQSSASTVPTVVCNGREVLDTSTSS 878

RESULT 6  
 JC7160  
 metabotropic glutamate receptor subtype 3 precursor - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 11-May-2000  
 C:Accession: JC7160  
 R:Minoshima, T.; Nakanishi, S.  
 J. Biochem. 126, 889-896, 1999  
 A:Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3  
 A:Reference number: JC7160, MUID:20012997, PMID:10544282  
 A:Accession: JC7160  
 A:Molecule type: DNA  
 A:Residues: 1-879 <MIN>  
 A:Cross-references: GB:AF170696  
 C:Genetics:  
 A:Gene: mGluR3  
 C:Superfamily: metabotropic glutamate receptor 4  
 C:Keywords: differentiation; G protein-coupled receptor; receptor; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-879/Product: metabotropic glutamate receptor subtype 3 #status predicted <MAT>  
 F:577-599/Domain: transmembrane #status predicted <TM1>  
 F:614-634/Domain: transmembrane #status predicted <TM2>  
 F:646-664/Domain: transmembrane #status predicted <TM3>  
 F:689-709/Domain: transmembrane #status predicted <TM4>  
 F:735-756/Domain: transmembrane #status predicted <TM5>  
 F:770-791/Domain: transmembrane #status predicted <TM6>  
 F:804-828/Domain: transmembrane #status predicted <TM7>

Query Match 21.0%; Score 1137; DB 2; Length 879;  
 Best Local Similarity 32.1%; Pred. No. 7.1e-75;

Matches 295; Conservative 152; Mismatches 361; Indels 112; Gaps 29;  
 33 KGDIIILGGLFFTHFGVAAKQDQLKSRPEATKCIYRN-PRGFRWLQAMIFAIEEINNSMTF 91  
 36 EGDVLGGLFFPN-----EKGTEECRCGNEDEGRIORLEAMLFAIDEINKDNVL 85  
 92 LPNITLGYRIFPTQNTVSKALEATISFV--ANKIDSLNL-----DEFNCSDHIPSTIA-V 145  
 86 LPGVKLVGHILDCSRDTYALEQSLFEFVRASITKVEAEYMCPCDGSYAIQENIPILLIAGV 145  
 146 VGNATSGSISTAVANLLGLEVIPOVSVASSRLLSNKNYKAFRLTIPINDEQQAATAAEII 205  
 146 IGSYSVSIQVANLLRLFCIFQISYASTSAKLSKSRDYFARTVPPDFYQAKMAEIL 205  
 206 EHPQMWVGTLAADDDYGRPGIDKFREEAVKRDICIDPSEMISQYTKQLE-FIADVIQ 264  
 206 RYENYIVTVTASVSEGYGETGIEAPEQEARLNICIATAEKVGRNIRKSYDSVIRELIQ 265  
 265 NSAKVIVVPSNGPDLPLIOIVRNITDRITLASEAWASSSLIAKPYFHVVGTTIGF 324  
 266 KPNARVVVLFMRSDDSRELIAAASRYN-ASFVTWASDGGWGAQESIVKGE-HVAYGAILT 323  
 325 ALRAGRIPGFNKFLKVPKSRSDNGFVKFEWEETNCFYFTEKTLTQLKNSKVPKSHGPA 384  
 324 ELASHPVRFQDRYFQSLNPNHRRNPFDRFWEQKFC-----SLQNR----- 367  
 385 QDGSKAGNSRRRTALRHPCTGEENTISVETPYLDYTHLRISYNYVAVYSIAHALQDIHS 444  
 368 -----NHRQICDKHLAIDSSN-----YEQESKIMFVN---AVYAMAHALHMKOR 409  
 445 --CKPGTGIFANGSCADIKKVEAWQVLNHLHLKFTNSMGEQ-----VDFDQDGLKGN 496  
 410 TLCPTNTKLCDAMKILDGKKL-----YKDYLLKINFAPFNPKNKAGDSIVKFDYIGDMGR 465  
 497 YTIINWQLSAEDBSVLFHEVGNYNAYAKP---SDRLNINEKKILWGFSGKVPFNSCRD 553  
 466 YNVFN-----FQHIGGKYSYLKVGHWAETLYLDVDSIHWGRNS--VPTSCSDP 512  
 554 CVPGRKRIIEGEPCTCFECMACAEGFSDENDASACTKCPNDFWSENHTSCIAKEIEY 613  
 513 CAPNEMKNMQPGD-VCCWICICEPEYEL--VDEFTCMDCGPGQWPTADLSGCYNLPEDY 569  
 614 LSWTEPFGIALTIFAVLGLITISFVLGVIKFNTPIVKATNRELSYLLFSLICCFSSS 673  
 570 IRWEDAWAIGPVTIACGLFMCTCIVTFIKHNTPLVKASGRELCCYLLFGVSLSYCMT 629  
 674 LIFIGEPDWTCELQROPAGISFVLICISILVNTNRLVLLVFEAKIPTSLHRKQWVGLNLOF 733  
 630 FFFIAKPSVICALRLRLGLTGFALCISVALLTKTNCIARIFDGVKGAQRPKFISSSQ- 688  
 734 LLVFLC---ILVQIVTCIIWLYTAPSSYRNHELED--EVIFITC---DEGSLMALGFLI 785  
 689 --VFICLGLILVQIVWVSVLILETPTGT-RRYTLPEKRETVILKCNVKSMLISL----- 741  
 786 GYTCLLAAICFFFAFKSRKLPENFNEAKFTIFGMLIFFIWIWISFIYAYVSTYKGF--VSA 843  
 742 TYDVVLVILCTVYAFKTRKCPENFNEAKFIFTWYTTTCIIWLAFPIFYVTSDDYRVQTT 801  
 844 VEVTAIALASFGILGCIYFNKCVIIILFKPCENTIEEVRCSSTAHAFAKVAARATLRRSA 903  
 802 TMCISVLSGFGVGLCLFAPKXHVILFQPKQNVVTH---RLHLNRFVSCTATYQSSA 858  
 904 RKRSSSLG-----STISS 917  
 859 STYVPTVVCNGREVLDTSTSS 878

RESULT 7  
 JH0563  
 metabotropic glutamate receptor 4 precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C:Accession: JH0563; I58149

Query Match	20.6%;	Score	1115.5;	DB 2;	Length	912;
Best Local Similarity	31.4%;	Pred.	No. 2.Re=73;			
Matches	293;	Conservative	167;	Mismatches	350;	Indels 123; Gaps 31;

  

QY	34	GDIIILGGIIFPHFGVAAQDOLKSRPEATCIRVNRGRFWLQAMIFATEINNNSMTLTP	93
DB	47	GDITLGGIIFPVH-----GRSGKACGLKK-----EKGIHRLKMLFALDRINDPDLLP	97
QY	94	NTLGVRIPTDCTNTVSKALEATLSFVAQNKIDSLNLDPCNSDHP-----STIAVVG	147
DB	98	NITLGARILDTCSRDTHALEQSLTFV-QALIEXDGTVEVRCG-SGGPPIITKPERVVGIG	155
QY	148	ATGSGISAVANLACLFIPOVSVYASSRLLSNKNKYKAFLATIPNDSCQATAMAEIEH	207
DB	156	AGSGSVSWVANIURLFKIPOISVASTAPDLSNSRYDFSRVWPSDYTQAQWVDIVRA	215
QY	208	FOMNWVGTLAADDYGRPGIDKFREEAAVK-DICIDFSEMIQYVTKQLKF-----IADVI	263
DB	216	LKNWVYSTLSEGSVSGSVEAFIQKSRNGGVCIQAQVKIPR--EPTKGEFDKIIRLL	273
QY	264	QNSSAKVIWFSNGPDLEPIQEIVRNITDR-IWLASEAWSSSL-TAKPEYFHVVGCT	321
DB	274	ETSNARGHIIIFANEDDIRRVLEAARRANQTGHFPMWGSWSGSKAPVLRLE--EVAEGA	331
QY	322	IGFALRAGRIQFGNKFLKVEHPSRSSNG----FVKEPWEETFCNVFEKTLTOLKNSKV	377
DB	332	VTLIPKNSVGFDRYS-----SETLDNRRNRTWFAEFWEDPHCKLSHAKGSKHIK-	386
QY	378	PSHGPAAGDGSKAGNSRRTRALRHPTCTGEENITSVETPYLDTHLRIISYNVVAVYSIAH	437
DB	387	-----KCTNRERI--GQDSAYEQSGKVQF---VIDAVYAMGH	418
QY	438	ALQDTHS--CKPGTGIFANGSCADIKKVEAKQVNLHLHLEKFTNSWGQVDFDQGDGLG	495
DB	419	ALHVAHRDLC-PG-----RVGLCPRPMDPVGTQLLKVIYNVNFSGIAGNPVTFNENGDA	473
QY	496	NYTIINWOL-----SAADESVLFEHVGYNVAYAKPSDRNLNINEKKILWSGFSKVPFNSCR	552

Query Match 20.6%; Score 1114.5; DB 2; Length 872;



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RESULT 10
A49874
metabotropic glutamate receptor 7 - rat
N:Alternate names: metabotropic glutamate receptor mGluR7
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: A49874; 157954
J:Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi,
J. Biol. Chem. 269, 1231-1236, 1994
A:Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 coup
A:Reference number: A49874; MUID:94117433; PMID:8288585
A:Accession: A49874
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-915 <RES>
A:Cross-references: UNIPROT:P35400; GB:D16817; NID:G458728; PIDN:BA04092.1; PID:G459729
R:Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L.
Mol. Pharmacol. 45, 367-372, 1994
A:Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid
A:Reference number: I57954; MUID:94195260; PMID:8145723
A:Accession: I57954
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-915 <RE2>
A:Cross-references: EMBL:U06832; NID:G459657; PIDN:AAA20655.1; PID:G459658
C:Genetics:
A:Gene: mGluR7
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor

Query Match 20.2%; Score 1092.5; DB 2; Length 915;
Best Local Similarity 30.6%; Pred. No. 1.4e-71;
Matches 287; Conservative 163; Mismatches 374; Indels 115; Gaps 31;

QY 24 YGPNRAQKGGDIIIGLGFPIHFGVAQKQDLKSPKATKC---IRYNFRGFMQAMIF 80
DB 38 YAPHS-IRIEGDTVLGLLFPVH---AKG-----PSGVPCKDIKREN--GTHRLAEMLY 84
QY 81 AIEEINNSMTFPINTLGVRIEDTNTVSKALEATLSFVAQNKIDSLNIDFECNSDHP 140
DB 85 ALDQINSNLPNVLGRIARLDTCSDRYALQESLTFV-QALIQKDTSD--VRCINGEP 141
QY 141 -----STIAVVGATGSGISTAVANLLGLFIPQVSYASSRLLSNKNEYKAFRTIPN 193
DB 142 PVFVRKPVGVGASGSSVSMVANILRLFPQISYASTAPELSDRRYDFFSRVVP 201
QY 194 DQQQATMAEIIIEHFQWNVVGLAADDYGRPGIDKFREEAVKR-DICIDFSEMSIYYT 252
DB 202 DSFQAQMYDVKALGWNVYSLASEGSGYRGVSEFTQISKEAGGLCIAQSVRIPOERK 261
QY 253 QKQLEP---IADVIONSSAKVIVVFNPGDLEPLIQTETVRRN-IDTRIWLASEAWASSL 308
DB 262 DRTIDFDRIKQLLDTFNSRAVVI FANDEDIKQILAAKRAQDVGHFLVWSDSGSK-- 319
QY 309 IAKPEYFH--VVGCTIGFALRAGRIPGNKFLKEVHPGRSSDNGVKEFWETNFCYTE 366
DB 320 -INPLHQHEDIAEGAITIQKATVEGFDAYFTSRLTNLRNRRNVWFAEYWEENFNCKLT 378
QY 367 KTLTLQKNSVPSHGPAAGDGSKAGNSRRRTALRHPTCGEENITSVETPYLDYTHLRIS 426
DB 379 -----SSKEDTDR-----KCTGQERI-KGDSNYEQEGKVQF-- 410
QY 427 NTVAVYSIAHALQDIHS--CKPGTGIFANGSCADIKKVEAWQVNLHLHLKFTNSMGQ 484
DB 411 -VIDAVYMAHALHNNKDLCAHYRGV-----CPMEQAGGKLLKYIRHVNFGNSAGT 464
QY 485 VPDQDGLKGNVTIINWLSADESVLFHEVGNVNAVKPSDRININEKILKSGFSKV 544
DB 465 VNFNKGDAFGYDYFOYITTTNTP-----GYRLIGQWTDLOQLNIEDMQKGVRE 517
QY 545 VPFNSGSRDVPGRKGIIEGPTCCFECMAEGEFDENDASACTKCPNDFWSNENHT 604

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Db 518 IPSVSVCTLPCKQRKKTQKGP-CCWTCEPC-DG-YQYQFDEMTQCHCPYDORPNENRT 574
QY 605 SCIAKEIYLSWTEPFGIALTFIAVLGILITSVLGVFIKFRNTPIVKATNRELSYLLLF 664
DB 575 GCQNIPIIKLEWSPNAVIVPFLAMLGIATIFVMTATFIRYNDTPIVRASGRELSYVLLT 634
QY 665 SLICCCSSSLIFGEPRDWTCLRQAFGISFVLCSILVKNRVLVLYFEAKIPSLHR 724
DB 635 GIFLCYIITFLMAKPDVAVCSFRVFLGLMGCISYAALLTKNRIYRIFEQCKKSVTAP 694
QY 725 KMYGLNLQFLVLCILVQIVTCIIWLYTAPPS---SYRNHEL---EDEVIFITCDEGSL 778
DB 695 RLISPTSQLAITSSLSISVQLLVGFVFWGVDPPNIIIDYDEHKTMPQEQARGVLKCDITDL 754
QY 779 MALGFLIGYTCLAAATCFFPAFAKSKRLPENFNKAFTITSMILFFIIVWISFIPAYVSTVG 838
DB 755 QIICSL-GYISILLVMTCTVYAIKTRGVPEFNENAKPIGTMYTTCIVWLAFIPF---FG 810
QY 839 KFSVAVEV-----IAILASSFGLLGCYIPNKCIVILLFKPCRNTEIEVRCSAAHAFK 890
DB 811 TAQSAEKLYIQTTLTISNMLASVALGMLYKPKVILLIFHP-----ELNVQKRKSEK 864
QY 891 VAARATLRRSAARKRS-----SSLCGST-ISSPAS 920
DB 865 AVVTAATMSRLSHKPSDRNGEAKTELCEVNDPNPSPAA 903

RESULT 11
149142
metabotropic glutamate receptor 8 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49142
R:Duvoisin, R.M.; Zhang, C.; Ramonell, K.
J. Neurosci. 15, 3075-3083, 1995
A:Title: A novel metabotropic glutamate receptor expressed in the retina and olfactory bu
A:Reference number: I49142; MUID:95239344; PMID:7722646
A:Accession: I49142
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-908 <RES>
A:Cross-references: UNIPROT:P47743; EMBL:U17252; NID:G854728; PIDN:AAA68149.1; PID:G85472;
C:Genetics:
A:Gene: mGluR8
C:Superfamily: metabotropic glutamate receptor 4
C:Keywords: neurotransmitter receptor

Query Match 19.9%; Score 1077; DB 2; Length 908;
Best Local Similarity 30.3%; Pred. No. 1.8e-70;
Matches 290; Conservative 176; Mismatches 363; Indels 122; Gaps 32;

QY 14 TLLQSYNVSGYGNPQRAQKGGDIIIGLGFPIHFGVAQKQ-----DLKSRPEATKCIY 67
DB 26 TMMQRTSHQSEYAHISRLD--GDIIIGLGFVH---AKGERGVPCGDLKKE----- 70
QY 68 NFGFRLQAMIPAEIEINNSMTFLNITLGVRIFTCNTVSKALEATLSFVAQNKIDSL 127
DB 71 --KGIRLEAMLYADQNTKRPDLNLSNITLGVRIIDTCSDRYALQESLTFV-QALIEKD 127
QY 128 NLDFECNCSN---HLPSTIA-VVGATGSGISTAVANLLGLFIPQVSYASSRLLSNKN 182
DB 128 ASDVKCANGDPPIFTFDPKISGVIGAAASSVSMVANILFKIPQISYASTAPELSDNT 187
QY 183 EYKAFRTIPNDEQQATMAEIIIEHFQWNVVGLAADDYGRPGIDKFREEAVKRDI--- 239
DB 188 RYDFFSRVVPDSYQACAMVDIVTALGWNVYSLASEGNYGSGVEAFTQ--ISREIGV 245
QY 240 CIDFSEMSIYYTQKLE-FIADVIONSSAKVIVVFNPGDLEPLIQTETVRRNITDR-IW 297
DB 246 CIAQSKIPREPFGPEFKIIEKLETFNARAVIMFANEDDINGILRAAKLNQSGHFLW 305
QY 298 LASEAWASSSLIAKPY--FHVVGTTIGFALRAGRIPGNKFLKEVHPGRSSDNGVKEFVK 355

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Db 306 IGSWSGSK---IAPVYQOEIEAGAVTILPKRASIDGDFRYSRRTLANRRNVWPAEF 362  
 QY 356 WEETNCVFTEKLTQLKNSKVPSHGPAAGDGGKAGNSRRRTALRHPCTGEINTSVETP 415  
 Db 363 SEGNGFC-----KSGSHG-----KNSHKKTGLERAR-DSS 395  
 QY 416 YLDYTHLRISYVAVVAVYSIAHALODIHS--CKPGTGIFANGSCADIKKVEAWOVNLHL 473  
 Db 396 YEQEKVQF---VIDAVYSMAVALHNMKEIC-PG---YIGLCPRVVTDIGKELGYIR 447  
 QY 474 HLKFTNSNGEQVDFDQDGLKGNYYTIINQLSAEDESFLFHEVGNYNAYAKSPRLNINE 533  
 Db 448 AVNFNGSAGTPVTENENGADPGYDIFQYQIN--NKSTEYKIIGHW-----TNQLHLKV 499  
 QY 534 KKLWSGSKVVPFNSCSDCVGPRKGIIEGEPTCCPEWACAEGEFSDENDASACTKC 593  
 Db 500 EDMQWANEHTHPASVCSLPCPKGBRKTIVKGPV--CMWRCRC-EG-YNYQVDELSCELC 556  
 QY 594 PNDWFNSNHTSCIAKETEYLSWTEPPFGIALTIFAVLGILITFSVLGVFIKFRNTPIVKA 653  
 Db 557 PLDQRPINRTGCQRIPIIKLEWHSWAVVPLVAILGIIATTFFVIVTFVYNDTPIVRA 616  
 QY 654 TNRELSYLLSLICCFSSSLIFGEPRDWTCLRQPAFGISFVLCISILVKNRVLLV 713  
 Db 617 SGRELSYLLTGIFLCYSITFLMAAPDTIICSPRRIFLGLMCFSYAALTKNRIHRI 676  
 QY 714 FEAKIPTSLHRKWVGLNQLFVLFCILVQIVTCIIMLYTAPP-----SSYRNEHELEDE 767  
 Db 677 FEQKKSVTAPKIFSPASQLVITFSLISVQLLVFVWFVDPPTIIDYGEQRTLDPEN 736  
 QY 768 VIFITCDGSLMALGFLGYTCLLAAICFFPAFASKRLPENFNBAKFTFSMLFFIWI 827  
 Db 737 RGVLCXDISDL-SLICSLGYSTLLMVTCTVVAIKTRGVPEFNEAKPIGFTMYTTCIWL 795  
 QY 828 SFIPAVVSTYKGFVSABV-----TAILASSFGLGCIYENKCYIILPKPCRNTEE 879  
 Db 796 AFIPF----FGTAQAEKMYIQTTLTVMSLSASVSLGMLYMPKVYIIIFHPQNVQR 852  
 QY 880 VRCSTAHAFAKVAARATLRRSAARSR-----SSLCGSTISSPASST 922  
 Db 853 KR-----SFKAVVTAATMQSKLIQKGNDRPNGEVKSELCELS-LEITNTSST 896  
 RESULT 12  
 JC2131  
 metabotropic glutamate receptor 5 B - human  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 05-Jan-1996  
 C:Accession: JC2131  
 R:Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.  
 Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994  
 A:Title: Molecular cloning and the functional expression of two isoforms of human metabo  
 A:Reference number: JC2131; PMID:94197696; PMID:7908515  
 A:Accession: JC2131  
 A:Molecule type: mRNA  
 A:Residues: 1-1212 <MIN>  
 C:Comment: this protein is coupled to guanine nucleotide binding proteins.  
 C:Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein  
 F:580-604/Domain: transmembrane #status predicted <TM1>  
 F:617-637/Domain: transmembrane #status predicted <TM2>  
 F:644-664/Domain: transmembrane #status predicted <TM3>  
 F:694-714/Domain: transmembrane #status predicted <TM4>  
 F:738-759/Domain: transmembrane #status predicted <TM5>  
 F:773-794/Domain: transmembrane #status predicted <TM6>  
 F:803-827/Domain: transmembrane #status predicted <TM7>  
 Query Match 19.5%; Score 1056.5; DB 2; Length 1212;  
 Best Local Similarity 28.5%; Pred. No. 9e-69;  
 Matches 302; Conservative 196; Mismatches 422; Indels 139; Gaps 35;  
 QY 8 LLFGLFTLLQSNVSGYGNQR-----AOKKGDIIILGLFPDIHFGVAAKQDLKSRPATK 63  
 Db 4 LLILSVLLKKE-DVRGSAQSSERRVVAHPMGDIIGALFSVH-----HQPTVDKVKHERK 56

RESULT 13

A41939

G protein-coupled glutamate receptor - rat

QY 64 C--IRYNFRGRFRLQAMIFAIERINNSMTFLNITLGYRIFDTCNTVSKALEATLSPVAQ 121  
 Db 57 CGAVRQY-GIQREAWLHTLERINSDPTLLNITLGEIRDSCHWMSVALEOSIEFIRD 115  
 QY 122 NKIDSNLDFNCSDHIPST-----IAVVGATGSGISTAVANLLGLFYIQQVSYASS 174  
 Db 116 SLISSEEEGLVRCVDSGSSSFSPKPIGVIGPGSSVAIQVONLLQLFNIPQIAYSAT 175  
 QY 175 SRLLSKNNEYKALRTPNDQOQATAMABIIIEHFQNWVGTLLAADDDYGRPGIDKREBA 234  
 Db 176 SMDLSKTLFKYPMRVPSDAQARAWDIVKRYNWTYSVAHTEGNGESGEAEFKDWS 235  
 QY 235 VKRDICIDISEMISQVYTKOLEFIADVION--SSAKVIWFSNGPDLPLTOEIVRRNI 292  
 Db 236 AKEGICIASYKLYSNAGEQSPDKLKLKLTSLPKARVVACCEGVTVRGLLWAMERLGL 295  
 QY 293 T-DRIMLASAWASSLIAKPEYFHVVGTTIGFALRAGRIPGNKFLKEVHSPSSDNGF 351  
 Db 296 AGEFLLGSDGWARDYDVTGQREAVGG-ITIKLQSPDKWFPDDYLLKRLPETNHRNPW 354  
 QY 352 VKEFWEETENCY--FTEKTLTOLKNSKVPSHGPAAGDGGKAGNSRRRTALRHPCTGEEN 408  
 Db 355 FQEFWQHRFOCRLEGPPQ-----ENSKY-----NKTCSNLSLTKTH----- 390  
 QY 409 ITSVEPYLDYTHLRISYVYV--AVYSIAHALQDIH-SCKPGTGIFANGSCADIKVEA 465  
 Db 391 -----HVQDSKXGFINA.YSMAYGLHNMQMSLCPGYA---GLCDAMKPIDG 434  
 QY 466 WQVLNHLHLKFTNSNGEQVDDQDGLKGNYYTIINQLSAEDESFLFHEVGNYNAYAKP 525  
 Db 435 RKLLSMLKTNFTGVSQDITLEDNGDSPGRVEIMNFEMGKD-----YFDINVGWDNG 490  
 QY 526 SDRLTANEKKILWSGSKVVPFNSCSDCVGPRKGIIEGEPTCCPEWACAEGEFSDEN 585  
 Db 491 ELKMDDE---VMSKSNRIIR-SVCSEPCCKGQIKVIRKEVSCCWTCPCKENEY--VF 544  
 QY 586 DASACTKCPNDFWNSNHTSCIAKE:EYLSWTEPPFGIALTIFAVLGILITFSVLGVFIK 645  
 Db 545 DEYTKACQLGSMPTDGLTCDLIPQVYLRWGDPEPIAAVFAVLGLLATLFTVVVFIIY 604  
 QY 646 RNTPIVKATNRELSTLLSLICCFSSSLIFGEPRDWTCLRQPAFGISFVLCISILV 705  
 Db 605 RDTVPVKSRELCTYIILAGICLGLYCTCLIAKPKQIYCYLQRIIGIGLSPAMSYALVT 664  
 QY 706 KTNRVLLVF---BAKIPTSLHRKWVGLNQLFVLFCILVQIVTCIIMLYTAPPSSYRNH 762  
 Db 665 KTNRIARILAGSKKIKCTKKPR-FMSACAQLVIAFLICIQLGIIIVLFIMEPPDIMHDY 723  
 QY 763 ELEDEVIFITCDGSLMALGFL--IGYTCLLAAICFFPAFASKRLPENENEAKFTFSML 820  
 Db 724 PSIREV-YLICNTTN--LGWVTPLGYNGLLISCTFFYAFKTRNVNVPANFEAKYIAFTWY 779  
 QY 821 IFFIVNISFIPAYVSTYKGFVSABVAVIAILASSFGLGCIYENKCYIILPKPCRNTEE 880  
 Db 780 TTCIILWAFVPIYFGSNYKIITMCFVSLSLATV--ALGCMFVPKVYIILAKERNVRSAP 837  
 QY 881 RCTAAHAFKVAARATLRRSAARSRKSSSIC-----GSTISSPASSTCGPLTMMEMQR- 933  
 Db 838 TTSTV-----VRMHVGDGKSSSAASRSLVNLWTKRGSS-----GETLRYKDRRL 883  
 QY 934 -----CSTQKVSPGS-GTVTLSLSFEETGRYATLSRTARSNSADGRSGDDLPSR-- 982  
 Db 884 AQHSIEIEFTPKSGMNGGRATMSSS---NGKSVTWAQNEKSSR-----CGHLWQRLS 934  
 QY 983 ---HPOQGPQKC--EPQPANDARYKAAPTKGTLESPPG 1016  
 Db 935 IHINKENPNQTAIVKPPFKSTBSRLGPGRGAGGSAGG 973





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Db 296 GEFLLGSGWADRVDTGQYQREAVGG--ITIKLQSPDVKMFDDYYLKLRETNLRNPF 354
Qy 353 KEFWEETENCY---FTEKTLTOLKNSKVPFSGHPAAQGGQKAGNRRRTALRHPCTGEENI 409
Db 355 QEFWQHRFCRLGFAQ-----ENSKY-----NKTCSNLSLRLTH----- 389
Qy 410 TSVETPYLDYTHLRISYVYV--AVYSTAHALQDIH--SCKPGTGIFANGSCADIKKVEAW 466
Db 390 -----HVQDSKMGFVFNATYSMAYGLHNQMSLCPGYA-----GLCDAMKPIDGR 434
Qy 467 QVLNELLHLKFTNSGEOVDFDDQDGLKGNNTIINWLSAEDSVLFHEVGNVYAYAKPS 526
Db 435 KLLDSLMKTNFTGVSGDMILFDENGSDPGRYEIMNFKEMGKD----YFYINVGSDNGE 490
Qy 527 DLRLNNEKKILMFGSKVVPFNSCRSDCVPTGRKGIIEGPTCCPECWACAGGFSDEND 586
Db 491 LKWDDE---VMSKKNIIIR--SVCSEPCCKGQIKVIRKEVSCCWTCTPCKENEY--VFD 544
Qy 587 ASACTKCPNDPWSNHNHTSCIAKEIYLSWTEPFGIALTIPAVLGILITSFVLGVFIKFR 646
Db 545 EYTCACQLGSWPTDGLTCDLIPVQYLRWGDPEPIAAVVFACLGILLATLFTVVFIIYR 604
Qy 647 NTPVIAKTNRELKLSLLFCPSLCCFSSSLIFIGEPDWTCLRPQAFGFSFVLCSILV 706
Db 605 DTPVVKSSRELKCYIILAGICLGLCTCLIAKPKQIYCYLQRIKIGLSLPAWSYALVTK 664
Qy 707 TNRVLLVF---EAKIPTSILHRKWGLNQFLVFLVLCILVQVTCIILWLYTAPPSSYRNHE 763
Db 665 TNRIARILAGSKKIKCTKKPR--FMSACAQLVIAFILIQIQLGIIIVAFIMEPFDIMHDP 723
Qy 764 LEDEVIFITCDGSLMALGFL--IGYTCLLAAICFFFAFKSRKLPENFNEAKFITFMSLI 821
Db 724 SIREV-YLICNTN---LGVVTPGLYNGLLILSCITFYAFKTRNVPANFNEAKYIAFTMYT 779
Qy 822 PFIWISIFIPAVSYGYFVSAVEVAILASGFLGCIYFNKCVIILFKPCRNFTIEVR 881
Db 780 TCIIWLAFVPIYFGSNYKIITMCFVSLSATV--ALGCMFVPKVIYIILAKPERNVRSAFT 837
Qy 882 CSTAAHAFKVAARATLRSAASRKSSSI-----CGSTISSPASSTCGPGLTWBMQ 932
Db 838 TSTV-----VRMHVGDGKSSAASRSSLVNLWKRGSSETLSN-----GKSVTWAQN 887
Qy 933 RCST-----QKVSF-----GSG----- 944
Db 888 EKSTRGQHLWRLSVEINKENPNQTAIVKPPKSTENRGPGAAAGGSGPGVAGAGNAG 947
Qy 945 -TVT-----LSLSFRETGR-----YATLSRTARSENADGESGDDL 979
Db 948 CTATGGBPPDAGPKALYDVAEBSFPAAARPSRPSITLSHLGSA-----GRTDGDA 1003
Qy 980 PSRHH 985
Db 1004 PSLHSE 1009

RESULT 15
JC2132
metabotropic glutamate receptor 5 A - human
C:Species: Homo sapiens (man)
C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C:Accession: JC2132
R:Minakami, K.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994
A:Title: Molecular cloning and the functional expression of two isoforms of human metabo
A:Reference number: JC2131, MUID:94197696; PMID:7908515
A:Accession: JC2132
A:Molecule type: mRNA
A:Residues: 1-1180 <MIN>
C:Comment: This protein is coupled to guanine nucleotide binding proteins.
C:Keywords: Glycoprotein; neurotransmitter; receptor; transmembrane protein
F:580-604/Domain: transmembrane #status predicted <TM1>
F:617-637/Domain: transmembrane #status predicted <TM2>
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F:644-664/Domain: transmembrane #status predicted <TM3>
F:694-714/Domain: transmembrane #status predicted <TM4>
F:738-759/Domain: transmembrane #status predicted <TM5>
F:773-794/Domain: transmembrane #status predicted <TM6>
F:803-827/Domain: transmembrane #status predicted <TM7>
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Query Match 19-28; Score 1040; DB 2; Length 1180;

Best Local Similarity 27.7%; Pred. No. 1.4e-67;  
Matches 299; Conservative 197; Mismatches 435; Indels 150; Gaps 33;

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Qy 8 LLFLGFTLLQSYNVSGYGNQR---AQRKGDILGLFPIHFGVAAKQDQLKSREATK 63
Db 4 LLILSVLLKX--DVRSQAQSSERRVAHWPFGDIIIGALFSVH-----HQPTVDKVHERK 56
Qy 64 C--IRYNFRGRFLQAMIFAEISNNMFLPNITLGYRIFDTCNTVSKALEATLSFVAQ 121
Db 57 CGAVREQY-QIQRVEAMLHTLERINSDPTLLPNITLGCIRDSCHMSVALESIIFRD 115
Qy 122 NKIDSLNLDLFCNCSHIPST-----IAVVGATGSGI-STAVANLLGFIYIPQVSYASS 174
Db 116 SLISSEBEEGLVRCVDGSSSSFRSKPIVGVIGPGSSVAIQVONLLQLENIPQIAYSAT 175
Qy 175 SRLLSNKNKYKAFRLTIPNDEQOATAMAEIIHFQNWVGTLAADDYDGRPGIDKREBA 234
Db 176 SMDLSKTLFKYFMRVVPVSDAQARAMVDIVKRYNMTYVSAVTEGNYGESGNEAFKDM 235
Qy 235 VKDICIIDREMI SQYYTOKOLEFIADVIQ--SSAKVIVVFSNGPDLEPLICEIVERNI 292
Db 236 AKGICIAHSYKIKYSNAGEQSFDKLLKLTSHLPKARVACFCEGTVRGLIMAMERLGL 295
Qy 293 T-DRIMLASAWASSLIAPKEFYHVVGSTIGFALRAGRIPGFNKFKEVHPSSSDNGF 351
Db 296 AGEFLLGSDGWADRYDVTGQYQREAVGG--ITIKLQSPDVKMFDDYYLKLRETNRN 354
Qy 352 VKSEWETENCY---FTEKTLTOLKNSKVPFSGHPAAQGGQKAGNRRRTALRHPCTGE 408
Db 355 QEFWQHRFCRLGFAQ-----ENSKY-----NKTCSNLSLRLTH----- 390
Qy 409 ITSVEPYLDYTHLRISYVYV--AVYSTAHALQDIH--SCKPGTGIFANGSCADIKKVE 465
Db 391 -----HVQDSKMGFVFNATYSMAYGLHNQMSLCPGYA-----GLCDAMKPIDG 434
Qy 466 WQVLNELLHLKFTNSGEOVDFDDQDGLKGNNTIINWLSAEDSVLFHEVGNVYAYAKP 525
Db 435 RKLESIMKTNFTGVSGDMILFDENGSDPGRYEIMNFKEMGKD----YFYINVGSDNG 490
Qy 526 SDRLNNEKKILMFGSKVVPFNSCRSDCVPTGRKGIIEGPTCCPECWACAGGFSDE 585
Db 491 ELKMDDE---VMSKKNIIIR--SVCSEPCCKGQIKVIRKEVSCCWTCTPCKENEY--VF 544
Qy 586 DASACTKCPNDPWSNHNHTSCIAKEIYLSWTEPFGIALTIPAVLGILITSFVLGVFIK 645
Db 545 DEVTCACQLGSWPTDGLTCDLIPVQYLRWGDPEPIAAVVFACLGILLATLFTVVFII 604
Qy 646 RNTPIVIAKTNRELKLSLLFCPSLCCFSSSLIFIGEPDWTCLRPQAFGFSFVLCSILV 705
Db 605 RDPVVKSSRELKCYIILAGICLGLCTCLIAKPKQIYCYLQRIKIGLSLPAWSYALV 664
Qy 706 KTNRVLLVF---EAKIPTSILHRKWGLNQFLVFLVLCILVQVTCIILWLYTAPPSSYRN 762
Db 665 KTNRIARILAGSKKIKCTKKPR--FMSACAQLVIAFILIQIQLGIIIVAFIMEPFDIM 723
Qy 763 ELDEVIFITCDGSLMALGFL--IGYTCLLAAICFFFAFKSRKLPENFNEAKFITFMS 820
Db 724 PSIREV-YLICNTN---LGVVTPGLYNGLLILSCITFYAFKTRNVPANFNEAKYIAFT 779
Qy 821 IFIWMISIFIPAVSYGYFVSAVEVAILASGFLGCIYFNKCVIILFKPCRNFTIEV 880
Db 780 TTCIWLAFVPIYFGSNYKIITMCFVSLSATV--ALGCMFVPKVIYIILAKPERNVRSA 837
Qy 881 RCSTAAHAFKVAARATLRSAASRKSSSI-----CGSTISSPASSTCGPGLTWEM 931
Db 838 TSTV-----VRMHVGDGKSSAASRSSLVNLWKRGSSETLSN-----GKSVTWAQ 887
```

QY	932	QRCST-----OKVSEGSCTVTLSISFEETGRYATLSRTARSNSADGR-----	974
Db	888	NEKSSRGQHLWQRLSI---HINKENPNQTAIVIKFPKSTESRGLGPGRGAGSAGGVGA	944
QY	975	-----SGDDLPSRHHQGGPPQKCEPOPANDARYKAAPTKGTLESFPGGSKE	1019
Db	945	TGGAGCAGAGGPGPESPDAGPKALYDVAEAEHFPAP---ARPRSPITLSHRAGSAS	1001
QY	1020	R 1020	
Db	1002	R 1002	

Search completed: November 17, 2004, 11:58:39  
Job time : 79 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 17, 2004, 07:02:14 ; Search time 425 Seconds

1390.376 Million cell updates/sec  
(without alignments)

Title: US-10-016-496-2

Perfect score: 5410  
Sequence: 1 MAQLHCOLLFLGLTLLQSYN.....KGTLESQGSKERPTTMEET 1027

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters:	1825181
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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02:\*

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1: uniprot_sprot:*
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2: uniprot_trembl:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description	%
1	5410	100.0	1027	2	Q8U104	Q8U104	squalus aca	
2	4044.5	74.8	1078	1	CASR_HUMAN	P41180	homo sapien	
3	3999.5	73.9	1085	1	CASR_BOVIN	P35384	bos taurus	
4	3996	73.9	1079	1	CASR_RAT	P48442	rattus norv	
5	3986	73.7	1079	2	Q8OZÅ8	Q8OZa8	rattus norv	
6	3767.5	73.5	1079	1	CASR_MOUSE	Q9C936	mus musculus	
7	3728	68.9	941	2	Q6XAF1	Q6Xaf1	salmo salar	
8	3728	68.9	941	2	AAP79925	AAP79925	salmo sal	
9	3721	68.8	941	2	Q6XAF3	Q6Xaf3	salmo salar	
10	3721	68.8	941	2	AAP79923	AAP79923	salmo sal	
11	3705.5	68.5	940	2	Q90WL6	Q90wl6	sparus aura	
12	3644.5	67.4	940	2	Q73635	Q73635	figu rubrip	
13	3456	63.9	850	2	Q6XAF2	Q6Xaf2	salmo salar	
14	3456	63.9	850	2	AAP79924	AAP79924	salmo sal	
15	2707.5	50.0	783	2	Q8CDP3	Q8cdp3	mus musculus	
16	1879	34.7	880	2	Q73639	Q73639	figu rubrip	
17	1804	33.3	856	2	Q73638	Q73638	figu rubrip	
18	1790.5	33.1	854	2	Q73637	Q73637	figu rubrip	
19	1776.5	32.8	848	2	Q93553	Q93553	carassius a	
20	1772	32.8	912	2	Q70410	Q70410	mus musculus	
21	1683.5	31.1	501	2	Q8Eun7	Q8Eun7	homo sapien	
22	1611.5	29.8	854	2	Q6UNX3	Q6unx3	ictalurus p	
23	1611.5	29.8	854	2	AAQ64679	AAQ64679	ictalurus	
24	1583	29.3	875	2	Q73640	Q73640	figu rubrip	
25	1577.5	29.2	868	2	Q73636	Q73636	figu rubrip	
26	1558	28.8	844	2	Q93552	Q93552	carassius a	
27	1362	25.2	877	2	Q9PW88	Q9pw88	carassius a	
28	1344.5	24.9	928	2	Q8K426	Q8K426	mus musculus	
29	1335	24.7	928	2	Q70VB1	Q70vb1	rattus norv	
30	1335	24.7	928	2	CA059483	CA059483	rattus norv	
31	1329.5	24.6	926	2	Q8NHZ9	Q8nhz9	homo sapien	

## RESULT 1

```

Q8J104
ID Q8J104 PRELIMINARY; PRT; 1027 AA.
AC Q8J104;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calcium polyvalent cation receptor/salinity sensing protein.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hypnosqualia; Squaliformes; Squaloidei;
OC Squalidae; Squalus.
CX NCBI_TaxID=7797;
[1]
RN SEQUENCE FROM N.A.
RP
RC TISSUE=Kidney;
RX MEDLINE=22103704; PubMed=12093923;
RA Nearing J., Becka M., Quinn S., Hentschel H., Elger M., Baum M.,
RA Bai M., Chattopadhyay N., Brown E.M., Hebert S.C., Harris H.W.;
RT "Polyvalent cation receptor proteins (Cars) are salinity sensors in
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9231-9236(2002).
DR EMBL; AF406649; AAM7700.1; -.
DR HSSP; P23385; LEWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR011828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASENSINGR.
DR PRINTS; PR00249; GPCRMR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; UNKNOWN_1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
DR Receptor.
SC SEQUENCE. 1027 AA; 114412 MW; 189FF1E323B5B7C7 CRC64;

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	Query Match	100.08;	Score 5410;	DB 2;	Length 1027;
	Best Local Similarity	100.08;	Pred. No. 0;		
	Matches 1027;	Conservative	0;	Mismatches	0; Gaps
y	1	MAQLHCQLLFGLFTLLQSYNSVSGYGPQRAQKGGDILGGLPFTHFGVAAKQDQLKS	RP	60	
b	1	MAQLHCQLLFGLFTLLQSYNSVSGYGPQRAQKGGDILGGLPFTHFGVAAKQDQLKS	RP	60	
y	61	ATKCRYNFRGFRMLQAMIFAIEINNSMTPLNITLGYRIEDTCNTVSKALEATLSFVA		120	
b	61	ATKCRYNFRGFRMLQAMIFAIEINNSMTPLNITLGYRIEDTCNTVSKALEATLSFVA		120	

QY 121 QNKIDSLNDELFCNCSHDHPISTIAVVGATGSGISTAVANLLGLFIPQVSVASSRLLSN 180  
 Db 121 QNKIDSLNDELFCNCSHDHPISTIAVVGATGSGISTAVANLLGLFIPQVSVASSRLLSN 180  
 QY 181 KNEYKAFILTIENDEQOATAMAEIIEHPQWNVGTLAADDYGRGIDKPFEEAVKRDIC 240  
 Db 181 KNEYKAFILTIENDEQOATAMAEIIEHPQWNVGTLAADDYGRGIDKPFEEAVKRDIC 240  
 QY 241 IDPSEMISQYTKOLEFIADVIQNSSAKIVVFSNGPDLEPLIOEIVVRNITDRIMLAS 300  
 Db 241 IDPSEMISQYTKOLEFIADVIQNSSAKIVVFSNGPDLEPLIOEIVVRNITDRIMLAS 300  
 QY 301 EAWASSLIAKPEYFHVVGTTGFALRAGRIPGFNKFKEVHPSSSDNGFVKPEWETP 360  
 Db 301 EAWASSLIAKPEYFHVVGTTGFALRAGRIPGFNKFKEVHPSSSDNGFVKPEWETP 360  
 QY 361 NCYFTEKTLTOLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420  
 Db 361 NCYFTEKTLTOLKNSKVPESHGPAAGDGSKAGNSRRTALRHPCTGEENITSVETPYLDYT 420  
 QY 421 HLRISYNNVAVYSIAHALQDISHCKPGTGFANGSCADIKKVEAWQVNLHLKFTNS 480  
 Db 421 HLRISYNNVAVYSIAHALQDISHCKPGTGFANGSCADIKKVEAWQVNLHLKFTNS 480  
 QY 481 MGEQVDFDQDGLKGYNTIINQLSAEDSVLFHEVGNVNAVAKPSDRNLNKKILWSG 540  
 Db 481 MGEQVDFDQDGLKGYNTIINQLSAEDSVLFHEVGNVNAVAKPSDRNLNKKILWSG 540  
 QY 541 FSKVPFNSCSDVPGTRKGIIIEGPTCCFECMACAEGEFSNDASACTKCPNDFWSN 600  
 Db 541 FSKVPFNSCSDVPGTRKGIIIEGPTCCFECMACAEGEFSNDASACTKCPNDFWSN 600  
 QY 601 ENHTSCIAKEIYLSWTEPFGIALTIFAVGLIITSFVLGVFIFKRNTPIVKATNRELSY 660  
 Db 601 ENHTSCIAKEIYLSWTEPFGIALTIFAVGLIITSFVLGVFIFKRNTPIVKATNRELSY 660  
 QY 661 LLLFSLICCFSSLIPIGPRDWTCLROPAGISFVLCISCLVKNRVLVPEAKIPT 720  
 Db 661 LLLFSLICCFSSLIPIGPRDWTCLROPAGISFVLCISCLVKNRVLVPEAKIPT 720  
 QY 721 SLHRKWGVLNQLFVLCILVQIVTCIIMLYTAPPSSVRNHELEDEVIPTCDGSLMA 780  
 Db 721 SLHRKWGVLNQLFVLCILVQIVTCIIMLYTAPPSSVRNHELEDEVIPTCDGSLMA 780  
 QY 781 LGFLIGYTCLLAALICFFFAFKSRKLPENFNEAKFITESMLIFFIWIWISFIPAYVSTYKGF 840  
 Db 781 LGFLIGYTCLLAALICFFFAFKSRKLPENFNEAKFITESMLIFFIWIWISFIPAYVSTYKGF 840  
 QY 841 VSAVEVIALASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900  
 Db 841 VSAVEVIALASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900  
 QY 901 ASARKRSSILCGSTISSPASSTCGGLTWMORCSTOKVSGSGVITLSLFEETGRVAT 960  
 Db 901 ASARKRSSILCGSTISSPASSTCGGLTWMORCSTOKVSGSGVITLSLFEETGRVAT 960  
 QY 961 LSRTARSNSADGRSGDDLPSRHHQGGPPQKCEPOPANDARYKAAPTGTLESPPGSKER 1020  
 Db 961 LSRTARSNSADGRSGDDLPSRHHQGGPPQKCEPOPANDARYKAAPTGTLESPPGSKER 1020  
 QY 1021 PTTMEET 1027  
 Db 1021 PTTMEET 1027

RESULT 2

CASR\_HUMAN  
 ID CASR\_HUMAN STANDARD; PRT: 1078 AA.  
 AC P41180; Q13912; Q16108; Q16109; Q16110; Q16379;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid  
 DE Cell calcium-sensing receptor).  
 GN Name=CASR; Synonyms=GPRC2A, PCAR1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OK NCBI\_TaxID=9606;  
 RN [1] SEQUENCE FROM N.A.  
 RP Pearce S.H.S., Thakker R.V.;  
 RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
 RL [2] SEQUENCE FROM N.A.  
 RP TISSUE=Parathyroid;  
 RX MEDLINE=95279439; PubMed=7759551;  
 RA Garrett J.E., Capuano I.V., Hammerland L.G., Hung B.C., Brown E.M.,  
 RA Hebert S.C., Nemeth E.F., Fuller F.;  
 RT "Molecular cloning and functional expression of human parathyroid  
 RT calcium receptor cDNAs.";  
 RL J. Biol. Chem. 270:12919-12925(1995).  
 RN [3] SEQUENCE FROM N.A.  
 RP TISSUE=Kidney;  
 RX MEDLINE=95408281; PubMed=7677761;  
 RA Aida K., Koishi S., Tawata M., Onaya T.;  
 RT "Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from  
 RT human kidney.";  
 RL Biochem. Biophys. Res. Commun. 214:524-529(1995).  
 RN [4] SEQUENCE FROM N.A.  
 RP MEDLINE=96343808; PubMed=8756555;  
 RA Freichel M., Zink-Lorenz A., Holloschi A., Hafner M., Flockerzi V.,  
 RA Raue F.;  
 RT "Expression of a calcium-sensing receptor in a human medullary thyroid  
 RT carcinoma cell line and its contribution to calcitonin secretion.";  
 RL Endocrinology 137:3842-3848(1996).  
 RN [5] SEQUENCE OF 643-908 FROM N.A.  
 RP MEDLINE=96193893; PubMed=8613532;  
 RA Bikle D.D., Ratnam A., Mauro T., Harris J., Pillai S.;  
 RT "Changes in calcium responsiveness and handling during keratinocyte  
 RT differentiation. Potential role of the calcium receptor.";  
 RL J. Clin. Invest. 97:1085-1093(1996).  
 RN [6] VARIANTS FHH GLN-185; LYS-297 AND TRP-795.  
 RP MEDLINE=94094324; PubMed=7916660;  
 RA Pollak M.R., Brown E.M., Chou Y.-H.W., Hebert S.C., Marx S.J.,  
 RA Seimann B., Levi T., Seidman C.E., Seidman J.G.;  
 RT "Mutations in the human Ca(2+)-sensing receptor gene cause familial  
 RT hypocalcemic hypercalcaemia and neonatal severe hyperparathyroidism.";  
 RL Cell 75:1297-1303(1993).  
 RN [7] VARIANT ADH ALA-127.  
 RP MEDLINE=95179179; PubMed=7874174;  
 RA Pollak M.R., Brown E.M., Estep H.L., McLaine P.N., Kifor O., Park J.,  
 RA Hebert S.C., Seidman C.E., Seidman J.G.;  
 RT "Autosomal dominant hypocalcaemia caused by a Ca(2+)-sensing receptor  
 RT gene mutation.";  
 RL Nat. Genet. 8:303-307(1994).  
 RN [8] VARIANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227.  
 RP MEDLINE=95243222; PubMed=7726161;  
 RA Chou Y.-H.W., Pollak M.R., Brandi M.L., Toss G., Arnqvist H.,  
 RA Atkinson A.B., Papapoulos S.E., Marx S., Brown E.M., Seidman J.G.,  
 RA Seidman C.E.;  
 RT "Mutations in the human Ca(2+)-sensing-receptor gene that cause  
 RT familial hypocalcemic hypercalcaemia.";  
 RL Am. J. Hum. Genet. 56:1075-1079(1995).  
 RN [9] SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.  
 RP MEDLINE=95403641; PubMed=7673400;  
 RA Aida K., Koishi S., Inoue M., Nakazato M., Tawata M., Onaya T.;  
 RT "Familial hypocalcemic hypercalcaemia associated with mutation in the

CC	human Ca (2+)-sensing receptor gene.";	CC	hypoparathyroidism (FHH) [MIM:146200]. FHH is characterized by
CC	J. Clin. Endocrinol. Metab. 80:2594-2598(1995).	CC	hypocalcemia and hyperphosphatemia due to inadequate secretion of
CC	[10]	CC	parathyroid hormone. Symptoms are seizures, tetany and cramps.
CC	VARIANTS NSHPT LEU-227 AND TYR-582.	CC	-!- SIMILARITY: Belongs to the G-protein coupled receptor family 3.
CC	MEDLINE=96229293; PubMed=8675635.	CC	-----
CC	Pearce S.H.S., Trump D., Wooding C., Besser G.M., Chew S.L.,	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	Grant D.B., Heath D.A., Hughes I.A., Paterson C.R., Whyte M.P.,	CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC	Thakker R.V.;	CC	the European Bioinformatics Institute. There are no restrictions on its
CC	"Calcium-sensing receptor mutations in familial benign hypocalcemia	CC	use by non-profit institutions as long as its content is in no way
CC	and neonatal hyperparathyroidism.";	CC	modified and this statement is not removed. Usage by and for commercial
CC	J. Clin. Invest. 96:2683-2692(1995).	CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC	[11]	CC	or send an email to license@isb-sib.ch).
CC	VARIANTS FHH THR-116, HIS-681 AND SER-806, AND VARIANT SER-851.	CC	-----
CC	MEDLINE=96311554; PubMed=8733126;	CC	EMBL; X81086; CAA56990.1; -
CC	Baron J., Winer K.K., Yanovsky J.A., Cunningham A.W., Laue L.,	CC	EMBL; U20759; AAA86503.1; -
CC	Zimmerman D., Cutler G.B. Jr.;	CC	EMBL; U20760; AAA86504.1; -
CC	"Mutations in the Ca(2+)-sensing receptor gene cause autosomal	CC	EMBL; D50855; BAA09453.1; -
CC	dominant and sporadic hypoparathyroidism.";	CC	EMBL; S83176; AAB46873.1; -
CC	Hum. Mol. Genet. 5:601-606(1996).	CC	EMBL; S79217; AAB35262.2; -
CC	[12]	CC	EMBL; S68032; AAB29413.2; ALT_SEQ.
CC	VARIANT FHH ARG-174.	CC	EMBL; S68033; AAB29414.1; -
CC	MEDLINE=97442275; PubMed=9298824;	CC	EMBL; S68036; AAB29415.1; -
CC	Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laing N.G., Pullan P.T.,	CC	EMBL; S81755; AAD14370.1; -
CC	Ratajczak T.;	CC	HSSP; P23385; LEWK.
CC	"A novel mutation (L174R) in the Ca2+-sensing receptor gene associated	CC	Genew; HGNC:1514; CASR.
CC	with familial hypocalcemic hypercalcemia.";	CC	MIM; 601199; -
CC	Hum. Mutat. 10:233-235(1997).	CC	MIM; 145980; -
CC	[13]	CC	MIM; 239200; -
CC	VARIANT FHH VAL-616.	CC	MIM; 601199; -
CC	MEDLINE=99415602; PubMed=10487661;	CC	MIM; 146200; -
CC	Stock J.L., Brown R.S., Baron J., Coderre J.A., Mancilla E.,	CC	GO; GO:0005887; C:integral to plasma membrane; TAS.
CC	De Luca F., Ray K., Meicq M.V.;	CC	GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
CC	"Autosomal dominant hypoparathyroidism associated with short stature	CC	GO; GO:0004435; F:phosphoinositide phospholipase C activity; TAS.
CC	and premature osteoarthritis.";	CC	GO; GO:0006874; P:calcium ion homeostasis; TAS.
CC	J. Clin. Endocrinol. Metab. 84:3036-3040(1999).	CC	GO; GO:0005513; P:calcium ion sensing; TAS.
CC	[14]	CC	GO; GO:0007635; P:chemosensory behavior; TAS.
CC	VARIANT FHH GLU-557.	CC	GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
CC	MEDLINE=21603857; PubMed=11762699;	CC	GO; GO:0009653; P:morphogenesis; TAS.
CC	Nakayama T., Minato M., Nakagawa M., Soma M., Tobe H., Aoi N.,	CC	GO; GO:0001503; P:ossification; TAS.
CC	Kosuge K., Sato M., Ozawa Y., Kamatsuse K., Kokubun S.;	CC	InterPro; IPR001828; ANF_receptor.
CC	"A novel mutation in Ca2+-sensing receptor gene in familial	CC	InterPro; IPR000068; Ca_sens_receptor.
CC	hypocalcemic hypercalcemia.";	CC	InterPro; IPR000337; GPCR_Mgr.
CC	Endocrine 15:277-282(2001).	CC	Pfam; PF00003; 7tm_3; 1.
CC	-!- FUNCTION: Senses changes in the extracellular concentration of	CC	Pfam; PF01094; ANF_receptor; 1.
CC	calcium ions. The activity of this receptor is mediated by a G-	CC	PRINTS; PR00248; GPCRMR.
CC	protein that activates a phosphatidylinositol-calcium second	CC	PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
CC	messenger system.	CC	PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.	CC	PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
CC	-!- ALTERNATIVE PRODUCTS:	CC	PROSITE; PS02559; G_PROTEIN_RECEP_F3_4; 1.
CC	Event=Alternative splicing; Named isoforms=2;	CC	Query Match 74.8%; Score 4044.5; DB 1; Length 1078;
CC	Name=1;	CC	Best Local Similarity 74.0%; Pred. No. 2.5e-275;
CC	isoId=P41180-1; Sequence=Displayed;	CC	Matches 782; Conservative 86; Mismatches 138; Indels 51; Gaps 7;
CC	Name=2;	CC	-----
CC	isoId=P41180-2; Sequence=VSP_002035;	CC	Qy 1 MAQLHCQLLFLGFTLLQSYNVSGVPNOAKKGGDILGLGFPFHFGVAAKQDOLKSRPE 60
CC	-!- TISSUE SPECIFICITY: Found in kidney, but not in brain, lung,	CC	Db 1 MAFYSCCWVLLALT-----WHTSAYGPDQRAQKGGDILGLGFPFHFGVAAKQDOLKSRPE 56
CC	liver, heart, skeletal muscle, or placenta.	CC	-----
CC	-!- DISEASE: Defects in CASR are the cause of familial hypocalcemic	CC	Qy 61 ATKCYRNFGRFWLQAMIFAEIEINNSMTPLNITLGYRIFDTCNTVSKALEATLSFVA 120
CC	hypercalcemia, type 1 (FHH) [MIM:145980]; in which the receptor	CC	Db 57 SVECYRNFGRFWLQAMIFAEIEINNSPALLPNLTGLRYFDTCNTVSKALEATLSFVA 116
CC	has reduced activity. FHH is characterized by altered calcium	CC	-----
CC	homeostasis. Affected individuals exhibit mild or modest	CC	Qy 121 QNKIDSLNLDFFCNCSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSIVASSRLLSN 180
CC	hypercalcemia, relative hypocalcemia, and inappropriately normal	CC	Db 117 QNKIDSLNLDFFCNCSEHIPSTIAVVGATGSGVSTAVANLLGLFYIPQVSIVASSRLLSN 176
CC	PTH levels.	CC	-----
CC	-!- DISEASE: Defects in CASR are the cause of neonatal severe primary	CC	Qy 181 KNEYKAFLETIENDGQATMAEIEHFWKQNVGVTAAADDYDGPIDKFRFEAVKRDIC 240
CC	hypoparathyroidism (NSHPT) [MIM:239200]; in which the receptor	CC	Db 177 KNOFKSFRTIENDGQATMADILEYFRWNVGVTIAADDYDGPIDKFRFEAEERDIC 236
CC	has reduced activity. NSHPT is a rare autosomal recessive life-	CC	-----
CC	threatening disorder characterized by very high serum calcium	CC	Qy 241 IDFSEMISQYTKQLEFIADYQIYQNSAKVIVFNSGPDLE

301 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIIFGKNFKLKEVHPSSSDNGFVKPEWETP 360  
 297 EAWASSSLIAKPEYFHVVGTTIGFALRAGRIIFGKNFKLKEVHPSSSDNGFVKPEWETP 356  
 361 NCYFTTKTLTKNSKVPKSHGPAQDQSGKAGNSRRTALRHHCTEENITSVETPYLDYT 420  
 357 NCHLQEGAKGPL---PVDITFLRGHEESGDRFENS-STAFRPLCTGDEMISSEVETPYDIT 412  
 421 HLRISYNYVAVYSIAHALQDIHSCKPGTGIFANGSCADIKKVEAWQVNLHLLHKLFTNS 480  
 413 HLRISYNYVAVYSIAHALQDIYTCPLGRGLTNGSCADIKKVEAWQVNLHLLHKLFTNS 472  
 481 MGEQVDFDQDGLKGYNTIINWOLSAEDSVLFHEVGNVNAVAKPSDRNLNKKILMSG 540  
 473 MGEQVTFDQDGLKGYNTIINWOLSAEDSVLFHEVGNVNAVAKPSDRNLNKKILMSG 532  
 541 FSKVVPFNSCSDVPGTRKGIIEGPTCCFPCMACAEGEPDENDASACTKCPNDWSN 600  
 533 FSRVVPFNSCSDVPGTRKGIIEGPTCCFPCMACAEGEPDENDASACTKCPNDWSN 592  
 601 ENHTSCIAKEIYLSWTEPFGIALTFIVLGLITLTSFVLGVFKPRNTPIVKATNRELVS 660  
 593 ENHTSCIAKEIYLSWTEPFGIALTFIVLGLITLTSFVLGVFKPRNTPIVKATNRELVS 652  
 661 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLCISILVKTNRVLLVFEAKIPT 720  
 653 LLLFSLICCFSSSLIFIGEPDWTCLRQPAFGISFVLCISILVKTNRVLLVFEAKIPT 712  
 721 SLHRKMWGLNLOFLVFLCIVQITCIITWLYTAPPSSYRNHELEDEVFITCDEGSLMA 780  
 713 SFRKMWGLNLOFLVFLCIVQITCIITWLYTAPPSSYRNHELEDEVFITCDEGSLMA 772  
 781 LGFLIGYTCLLAAICFFFAFKRKLPEPNEAKPTFMSLFFIWIWISFIPAYSTYKGF 840  
 773 LGFLIGYTCLLAAICFFFAFKRKLPEPNEAKPTFMSLFFIWIWISFIPAYSTYKGF 832  
 841 VSAVEVIALASFGLLGCIYENKCVIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 900  
 833 VSAVEVIALASFGLLGCIYENKCVIILFKPCRNTEIEVRCSTAAHAFKVAARATLRS 892  
 901 AASRKRSSSLGSGTSSPASSTCGPG-----LNMEN 931  
 893 NVSRKRSSSLGSGTSSPASSTCGPG-----LNMEN 922  
 932 Q-----RCSTQKVSFGSGTTLTSLFTEGTGRVATLSRTARSNSADGRSGDDLPSRHH 984  
 953 QORSQQPCK-QKVFSGTTLTSLFTEGTGRVATLSRTARSNSADGRSGDDLPSRHH 1010  
 985 DQGPFPCKPQPPANDARYAAPTGTLSPPGSKERP 1021  
 1011 -----QPLLPLCGTDLDTLTVQETGLQGPVGGDQRP 1042

## RESULT 3

CASR\_BOVIN STANDARD; PRT; 1085 AA.  
 ID CASR\_BOVIN STANDARD; PRT; 1085 AA.  
 AC P35384;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid  
 DE Cell calcium-sensing receptor).  
 OS Name=CASR; Synonyms=GPRC2A, PCAR1;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Parathyroid;  
 RX MEDLINE=94077182; PubMed=8252596;

RA Brown E.M., Gamba G., Riccardi D., Lombardi M., Butters R., Kifor O.,  
 RA Sun A., Fediger M.A., Lytton J., Hebert S.C.;  
 RT "Cloning and characterization of an extracellular Ca(2+)-sensing  
 RT receptor from bovine parathyroid.";  
 RL Nature 366:575-580(1993).  
 CC -!- FUNCTION: Senses changes in the extracellular concentration of  
 CC calcium ions. The activity of this receptor is mediated by a G-  
 CC protein that activates a phosphatidylinositol-calcium second  
 CC messenger system.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor family 3.  
 CC  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 CC EMBL; S67307; AAB29171.1; -;  
 CC PIR; S40476; S40476.  
 CC HSP; P23385; IEWT.  
 DR InterPro; IPR001828; ANF\_receptor.  
 DR InterPro; IPR000069; Ca\_sens\_receptor.  
 DR InterPro; IPR000337; GPCR\_Mgr.  
 DR Pfam; PF00003; 7tm\_3; 1.  
 DR Pfam; PF01094; ANF\_receptor; 1.  
 DR PRINTS; PR0248; GPCRMR.  
 DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
 DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
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 KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.  
 FT SIGNAL 1 19  
 FT CHAIN 20 1085  
 FT DOMAIN 20 613  
 FT TRANSMEM 614 636  
 FT DOMAIN 637 650  
 FT TRANSMEM 651 671  
 FT DOMAIN 672 682  
 FT TRANSMEM 683 701  
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 FT DOMAIN 747 770  
 FT TRANSMEM 771 793  
 FT DOMAIN 794 806  
 FT TRANSMEM 807 829  
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 FT TRANSMEM 838 863  
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 FT CARBOHYD 91 91  
 FT CARBOHYD 131 131  
 FT CARBOHYD 262 262  
 FT CARBOHYD 288 288  
 FT CARBOHYD 401 401  
 FT CARBOHYD 447 447  
 FT CARBOHYD 469 469  
 FT CARBOHYD 489 489  
 FT CARBOHYD 542 542  
 FT CARBOHYD 595 595  
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 Query Match 73.9%; Score 3999.5; DB 1; Length 1085;  
 Best Local Similarity 72.8%; Pred. No. 3.7e-272;  
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 QY 1 MAQLHCQLFLGFTLLQSYNVSQYGNQRAQKGGIILGLFPFHGVAAKDQDLKSRE 60  
 Db 1 MALYSCCWILLAFS---TWCTSAQYDQRAQKGGIILGLFPFHGVAQDQDLKSRE 57  
 QY 61 ATKICIRYNGFRWLOQMFAIEEINNSMTFLPNITLGVRIFDTCNTVSKALEATLSVA 120



58 SVEGIRVFRGRWLQAMFAIEBINSPPALLPNMTLGYRIFDTCNTVSKALEATUSFVA 117  
121 QNKIDSLNLDNDFCNCSHPISTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 180  
118 QNKIDSLNLDNDFCNCSHPISTIAVVGATGSGISTAVANLLGLFYIPOVSYASSRLLSN 177  
181 KNEYKAFRLTIPNDEQQATAMAEIIEHFQWVWGTAAADDDYGRPGIDKFREEAVKEDIC 240  
178 KNQFKSPLRTIPNDEHQATAMADIEYPRWVWGTIAADDDYGRPGIEKFREEAEERDIC 237  
241 IDFSMISQYQKOLEFIADVIONSSAKVIVFNSGPDLEPLCEIVRRNITRIWLAS 300  
238 IDFSBELISQYDEEIKQIVVEIONSTAKVIVFSSGPDLEPLKEIVRRNITRIWLAS 297  
301 EAWASSSLIAKPEYHVHVGGTIGFALRAGRIPGFNKFELKEVHPSRSSDNGFVKFEWETP 360  
298 EAWASSSLIAKPEYHVHVGGTIGFGLKAGQIPGFREFLQKVHPRKSVHNGFAKFEWETP 357  
361 NCYFTEKTLTOLKNSKVPSSHGPAAGDQSGKAGNSRRTALRHPCTGEENITVETPYLDYT 420  
358 NCHLQEGAKGPL---PVDFTLRGHEGGARLSNS--PTAFRPLCTGGEENISVETPYMDYT 413  
421 HLRISYVWVAVYSTAHALQDTHSCPKGTGIFANGSCADIKKVEAWQVNLHLLHLKFTNS 480  
414 HLRISYVWVAVYSTAHALQDTHSCPKGTGIFANGSCADIKKVEAWQVNLHLLHLKFTNS 473  
481 MGEQVDFDDQDGLKGNYYTIINWLSAEDSVLFHEVGNYNAYAKPSDLNINEKKILMSG 540  
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541 ESKVVPFNSCSDCVPGTKGIIIEGPTCCPEMACAESEDSNDASACTKCPNDPWSN 600  
534 FSEVPFNSCSDCVPGTKGIIIEGPTCCPEMACAESEDSNDASACTKCPNDPWSN 593  
601 ENHTSCIAKEIENWTEPFGIALTIFAVLGLILTSFVLGVFIKPRNTPIVKATNRELSY 660  
594 ENHTSCIAKEIENWTEPFGIALTIFAVLGLILTSFVLGVFIKPRNTPIVKATNRELSY 653  
661 LLLFSLICFSSSLPIGEPRDWTCLROPARGISFVLCISILVKNRVLVFEAKIPT 720  
654 LLLFSLICFSSSLPIGEPRDWTCLROPARGISFVLCISILVKNRVLVFEAKIPT 713  
721 SHHRKWGNLQFLAVFLCIVQITCIILWLTAPPSSVYRNHELEDEIVFITCDGSLMA 780  
714 SHHRKWGNLQFLAVFLCIVQITCIILWLTAPPSSVYRNHELEDEIVFITCDGSLMA 773  
781 LGFLIGYTCLLAACIFFFAFKSRKLPENFNEAKFITFSMLIFFIWMISFIPAYASTYKGF 840  
774 LGFLIGYTCLLAACIFFFAFKSRKLPENFNEAKFITFSMLIFFIWMISFIPAYASTYKGF 833  
841 VSAVEVIALASFGILGCIYFNKCVIILFKPCRNTEIEVRCTAAHAFKVAARATLRS 900  
834 VSAVEVIALASFGILGCIYFNKCVIILFKPCRNTEIEVRCTAAHAFKVAARATLRS 893  
901 AASRKRSSSLCGSTISSPASSTCG-----P 925  
894 NVSRQSSSLGSGTGTSPSSISSKNSDEPPDQQQPKQKQPQLALSPHNAQQPQPR 953  
926 GLTMEVQ-----RGTQKVSFGSTVLSLFSFTGYATLSRTARENSADGESGD 978  
954 PSTPQPOSQPPRCK-QKVIKSGTIVTSLSFDEPQKTAHARNSTHQTSLAQKND 1012  
979 LPSRHHQDQPPKCEPOPANDARYKAAPTGTLESPPGSKERTPTTME 1026  
1013 ALTKH-----QALLPQCGTDSLTQSQETGLQGPVG-EDHOLEMED 1053

RESULT 4  
CASR RAT  
ID\_CASR RAT  
AC P48442; 1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)  
Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid  
Cell calcium-sensing receptor).  
Name=Casr; Synonyms=Gprc2a, Pcarl;  
Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
CX NCBI\_TaxID=10116;  
[1]  
SEQUENCE FROM N.A.  
RP STRAIN=Gawley; TISSUE=Kidney outer medulla;  
RC MEDLINE=95116508; PubMed=7816802;  
RX Riccardi D., Park J., Lee W., Gamba G., Brown E.M., Hebert S.C.;  
RA "Cloning and functional expression of a rat kidney extracellular  
RT calcium/polyvalent cation-sensing receptor".  
RL Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995).  
[2]  
SEQUENCE OF 1-294 FROM N.A.  
RP STRAIN=Mistar;  
RC MEDLINE=95241465; PubMed=7724534;  
RX Ruat M., Snowman A.M., Snyder S.H.;  
RA "Calcium sensing receptor: molecular cloning in rat and localization  
RT to nerve terminals".  
RL Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).  
CC -1- FUNCTION: Senses changes in the extracellular concentration of  
CC calcium ions. The activity of this receptor is mediated by a G-  
CC protein that activates a phosphatidylinositol-calcium second  
CC messenger system.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor family 3.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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EMBL; U10354; AAC52149.1; -;  
EMBL; U20289; AAC52195.1; -;  
PIR; I59362; I59362.  
DR HSSP; P23385; LEWK.  
RGD; 2277; Casr.  
DR InterPro; IPR001828; ANF\_receptor.  
DR InterPro; IPR000068; Ca\_sens\_receptor.  
DR InterPro; IPR000337; GPCR\_Mgr.  
DR Pfam; PF00003; 7tm\_3; 1.  
DR Pfam; PF01094; ANF\_receptor; 1.  
DR PRINTS; PR00248; GPCRMR.  
DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
DR PROSITE; PS0259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.  
FT SIGNAL 1 19  
FT CHAIN 20 1079  
FT DOMAIN 20 612  
FT TRANSMEM 613 635  
FT DOMAIN 636 649  
FT TRANSMEM 650 670  
FT DOMAIN 671 681  
FT TRANSMEM 682 700  
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FT DOMAIN 746 769  
FT TRANSMEM 770 792  
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FT TRANSMEM 806 828  
FT DOMAIN 829 836  
FT TRANSMEM 837 862  
FT DOMAIN 863 1079  
FT CARBOHYD 90 90  
Extracellular calcium-sensing receptor.  
Extracellular (Potential).  
1 (Potential).  
Cytoplasmic (Potential).  
2 (Potential).  
Extracellular (Potential).  
3 (Potential).  
Cytoplasmic (Potential).  
4 (Potential).  
Extracellular (Potential).  
5 (Potential).  
Cytoplasmic (Potential).  
6 (Potential).  
Extracellular (Potential).  
7 (Potential).  
Cytoplasmic (Potential).  
N-linked (GlcNAc...) (Potential).

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FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 261 261 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 287 287 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 386 386 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 446 446 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 468 468 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 541 541 N-linked (GlcNAc...) (Potential)
FT CARBOHYD 594 594 N-linked (GlcNAc...) (Potential)
SQ SEQUENCE 1079 AA; 120867 MW; D7664550361F9736 CRC64;

Query Match
Best Local Similarity 73.9%; Score 3996; DB 1; Length 1079;
Matches 780; Conservative 85; Mismatches 140; Indels 54; Gaps 8;

QY 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLPFIHFGVAAKDQDLKSRPE 60
DQ 1 MASYSCLALLAL---AWHSSAYGPDQRAQKGGDIILGGLPFIHFGVAAKDQDLKSRPE 56
61 ATKCIYRNGRFRWLQAMIFAIETENNMTLPNTITLGYRIEDTCTNTVSKALEATLSFVA 120
DQ 57 SVCEIYRNGRFRWLQAMIFAIETENNMTLPNTITLGYRIEDTCTNTVSKALEATLSFVA 116
QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGTAVANLLGLFYIPQVSYASSRLLSN 180
DQ 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGTAVANLLGLFYIPQVSYASSRLLSN 176
QY 181 KNEYKAFRTINDEQCATAMAEIIEHFQWNVGTLAADDYGRGIDKFEAEAVKRDIC 240
DQ 177 KNEYKAFRTINDEQCATAMAEIIEHFQWNVGTLAADDYGRGIDKFEAEAEERDIC 236
241 IDFSEMISQYTKQLEFIADYQNSAKVIVFSSNGPDLELIQEIIVRNITDRIMLAS 300
DQ 237 IDFSELSIQSYDEEIQVVEIQNSAKVIVFSSNGPDLELIQEIIVRNITDRIMLAS 296
QY 301 EAWASSILLAKPEYFHVUGGTGTFALRAGRIKPGFNKFLKEVHPSSSSNGFVGFWEETF 360
DQ 297 EAWASSILLAKPEYFHVUGGTGTFALRAGRIKPGFNKFLKEVHPSSSSNGFVGFWEETF 356
QY 361 NCYFTEKTLTQK-LNSKVPSHGPAAGDGSKAGNSRTALRHPCTGGEENITSVETPYLDY 419
DQ 357 NCHLQEGAKPLPVDTFVRSH---EEGNRLNLS-STAFPLCTGGEENITSVETPYNDY 411
QY 420 TRLRSYNNVYVAVYIAHALQDIHCKPGTGIIFANGSCADIKKVEAWQVNLHLLKFTN 479
DQ 412 EHLRSYNNVYVAVYIAHALQDIYTCLEPGLFTNGSCADIKKVEAWQVNLHLLKFTN 471
QY 480 SMGEQVDFDDQGLKGNITINWQISAEDESVLFEVGNVYNAKPSDLNINEKILWS 539
DQ 472 NMGEQVDFDECDLGNVTSINWHLSPEDGSIVFKEVGYNNVYAKKGRLEFINSEKILWS 531
QY 540 GFSKVVPFNSCRDCVPGTRKGIIEGPTCCFECMACAEGFSDENASACTKCPNDFWS 599
DQ 532 GFSREVPFNSCRDCQAGTRKGIIEGPTCCFECVCEPCDGEYSGETDASACDKCPDFFWS 591
QY 600 NENHTSCAKETIYLSWTEPGIATITFVILGILITSVLGVFKFRNTPIVKATNELS 659
DQ 592 NENHTSCAKETIYLSWTEPGIATITFVILGILITSVLGVFKFRNTPIVKATNELS 651
QY 660 YLLFLSLCCFSSSLIFIGEPRDWTCLRQAPAGISFVLICISILVKNRVLVFEAKIP 719
DQ 652 YLLFLSLCCFSSSLIFIGEPRDWTCLRQAPAGISFVLICISILVKNRVLVFEAKIP 711
QY 720 TSLHRKWGLNLQFLVFLCILLVQIVTCIIWLYTAPSSSYRNHELEDEVIPTCDEGLM 779
DQ 712 TSFHRKWGLNLQFLVFLCILLVQIVTCIIWLYTAPSSSYRNHELEDEVIPTCDEGLM 771
QY 780 ALGFLIGYTCLLAA-CFFPFAFKSKLPENFNEAKFITPSMLIFPIVWISFIPAVVSTYK 839
DQ 772 ALGSLIGYTCLLAA-CFFPFAFKSKLPENFNEAKFITPSMLIFPIVWISFIPAVVSTYK 831
QY 840 FVSAVEVIAIALASSFGLGCIYFNKCYIILPKPCNTIEEVRCSAAAHAFKVAARATLRR 899

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832 FVSAVEVIAIALASSFGLGCIYFNKCYIILPKPCNTIEEVRCSAAAHAFKVAARATLRR 891
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892 PNISRKSSSLGSGTSGIPSSSSSKNSNEDRPQEPQKQQQLSLTQEQQQQLTLH 951
931 MQ-----RCSTQKVSFGSGVTLSLFEETGRVATLSRTARSNSADGRSGDDLPSR 982
952 PQQQQQPQPRCK-QKVIFSGVTLSLFEDEPKNAMAHNSMRQNSLEAQRSDNTLGR 1010
983 HHDGQPPQKCEPOPANDARYKAAPTKGTLESPPGSKERP 1021
1011 H-----QALLPQCADADSEMTIOETGLQGPVWDHQP 1043

PRT; 1079 AA.

AC Q80ZA8; PRELIMINARY;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Calcium sensing receptor.
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [.]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Dorsal root ganglion;
RA Bukoski R., Bian K., Wang Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY214122; AAO59490.1;
DR HSP; P23385; IWK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto...; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000068; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASSENSINGR.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
DR PROSITE; PS02559; G_PROTEIN_RECEP_F3_4; 1.
KW Receptor.
SQ SEQUENCE 1079 AA; 120830 MW; 50A2D026AE65CE81 CRC64;

Query Match 73.7%; Score 3986; DB 2; Length 1079;
Best Local Similarity 73.5%; Pred. No. 3.3e-271;
Matches 778; Conservative 87; Mismatches 140; Indels 54; Gaps 8;

QY 1 MAQLHCOLLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLPFIHFGVAAKDQDLKSRPE 60
DQ 1 MASYSCLALLAL---AWHSSAYGPDQRAQKGGDIILGGLPFIHFGVAAKDQDLKSRPE 56
61 ATKCIYRNGRFRWLQAMIFAIETENNMTLPNTITLGYRIEDTCTNTVSKALEATLSFVA 120
DQ 57 SVCEIYRNGRFRWLQAMIFAIETENNMTLPNTITLGYRIEDTCTNTVSKALEATLSFVA 116
QY 121 QNKIDSLNDEFNCSDHIPSTIAVVGATGSGTAVANLLGLFYIPQVSYASSRLLSN 180
DQ 117 QNKIDSLNDEFNCSEHIPSTIAVVGATGSGTAVANLLGLFYIPQVSYASSRLLSN 176
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DQ 177 KNEYKAFRTINDEQCATAMAEIIEHFQWNVGTLAADDYGRGIDKFEAEAEERDIC 236
177 KNEYKAFRTINDEQCATAMAEIIEHFQWNVGTLAADDYGRGIDKFEAEAEERDIC 236
241 IDFSEMISQYTKQLEFIADYQNSAKVIVFSSNGPDLELIQEIIVRNITDRIMLAS 300
DQ 237 IDFSELSIQSYDEEIQVVEIQNSAKVIVFSSNGPDLELIQEIIVRNITDRIMLAS 296
QY 301 EAWASSILLAKPEYFHVUGGTGTFALRAGRIKPGFNKFLKEVHPSSSSNGFVGFWEETF 360
DQ 297 EAWASSILLAKPEYFHVUGGTGTFALRAGRIKPGFNKFLKEVHPSSSSNGFVGFWEETF 356
QY 361 NCYFTEKTLTQK-LNSKVPSHGPAAGDGSKAGNSRTALRHPCTGGEENITSVETPYLDY 419
DQ 357 NCHLQEGAKPLPVDTFVRSH---EEGNRLNLS-STAFPLCTGGEENITSVETPYNDY 411
QY 420 TRLRSYNNVYVAVYIAHALQDIHCKPGTGIIFANGSCADIKKVEAWQVNLHLLKFTN 479
DQ 412 EHLRSYNNVYVAVYIAHALQDIYTCLEPGLFTNGSCADIKKVEAWQVNLHLLKFTN 471
QY 480 SMGEQVDFDDQGLKGNITINWQISAEDESVLFEVGNVYNAKPSDLNINEKILWS 539
DQ 472 NMGEQVDFDECDLGNVTSINWHLSPEDGSIVFKEVGYNNVYAKKGRLEFINSEKILWS 531
QY 540 GFSKVVPFNSCRDCVPGTRKGIIEGPTCCFECMACAEGFSDENASACTKCPNDFWS 599
DQ 532 GFSREVPFNSCRDCQAGTRKGIIEGPTCCFECVCEPCDGEYSGETDASACDKCPDFFWS 591
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DQ 652 YLLFLSLCCFSSSLIFIGEPRDWTCLRQAPAGISFVLICISILVKNRVLVFEAKIP 711
QY 720 TSLHRKWGLNLQFLVFLCILLVQIVTCIIWLYTAPSSSYRNHELEDEVIPTCDEGLM 779
DQ 712 TSFHRKWGLNLQFLVFLCILLVQIVTCIIWLYTAPSSSYRNHELEDEVIPTCDEGLM 771
QY 780 ALGFLIGYTCLLAA-CFFPFAFKSKLPENFNEAKFITPSMLIFPIVWISFIPAVVSTYK 839
DQ 772 ALGSLIGYTCLLAA-CFFPFAFKSKLPENFNEAKFITPSMLIFPIVWISFIPAVVSTYK 831
QY 840 FVSAVEVIAIALASSFGLGCIYFNKCYIILPKPCNTIEEVRCSAAAHAFKVAARATLRR 899

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241 IDSEMI:SQYTKQLEFIADVIQNSAKVIVVFSNGPDLEPLIOETVRRNITDRWLAS 300  
 237 IDPSEL:SQYDEBEIQOWEVIQNSAKVIVVFSNGPDLEPLIOETVRRNITGRWLAS 296  
 301 EAWASSLI:KPEYTHVVGTTGIGALBAGRI:PGNKELKVEHPSSDNGDFVKEFWETP 360  
 297 EAWASSLI:KPEYTHVVGTTGIGALBAGRI:PGNKELKVEHPSSDNGDFVKEFWETP 356  
 361 NCYFTEKTLTKL:NSKVPSSGPAAGDGSKAGNSRRTALRHPCGTGENITSVETPYLDY 419  
 357 NCHLOEGAKG:PLPVDTFVRSH:---EEGNNLLNS-STAFRPLCTGDNINSVETPYMDY 411  
 420 THLRISYNYVAV:SIHAHALODIHSXPGCTGIFANGSCADIKKVEAVQVNLHLHLFTN 479  
 412 EHLRISYNYVAV:SIHAHALODIHSXPGCTGIFANGSCADIKKVEAVQVNLHLHLFTN 471  
 480 SMGQVDDDDG:DLKGNVTIINWOLSADESVLFHEVGNVYNAKPSDRNLNINEKKILWS 539  
 472 NNGEQVTFDE:CGDLVGNYSIINWHLSPDGSIVKEVGYNNYAKKERUFINEEKILWS 531  
 540 GFSKVPFNSC:RDCVPOTRKGIIIEGPTCCFECMACAGBFSNDENASACTKPNDFWS 599  
 532 GFSREVPFNSC:RDCVPOTRKGIIIEGPTCCFECMACAGBFSNDENASACTKPNDFWS 591  
 600 NENHTSCIAK:IEVLSWEPFGIALTIFAVLIGLITSFVLGVTIKFRNTPIVKATNRELS 659  
 592 NENHTSCIAK:IEVLSWEPFGIALTIFAVLIGLITSFVLGVTIKFRNTPIVKATNRELS 651  
 660 YLLFSLIACC:SSSLIFIGERDWTCLRQPAFGISFVLC:SCILVKNRVLVLFKAKIP 719  
 652 YLLFSLIACC:SSSLIFIGERDWTCLRQPAFGISFVLC:SCILVKNRVLVLFKAKIP 711  
 720 TSLHRKVG:LNQFLVFLCIVLQVITCIILYTPAPSSYNHELEDEVIITCDEGLM 779  
 712 TSFHRKVG:LNQFLVFLCIVLQVITCIILYTPAPSSYNHELEDEVIITCDEGLM 771  
 780 ALGFLIGT:VTCLLAALCFPFAPKSKLIPENFNAKEITFMSLIFITVIFPXYSTYVGK 839  
 772 ALGSLIGT:VTCLLAALCFPFAPKSKLIPENFNAKEITFMSLIFITVIFPXYSTYVGK 831  
 840 FVSVEVIA:ILASSFGLGCIYFNKCYIILFKPCNTTIEVRCSTAAAFKVAARATLRR 899  
 832 FVSVEVIA:ILASSFGLGCIYFNKCYIILFKPCNTTIEVRCSTAAAFKVAARATLRR 891  
 900 SAASKR:SSLCGTSIIPASSTCGP:-----LTM 930  
 892 PNISKR:SSLCGTSIIPASSTCGP:-----LTM 951  
 931 MQ:-----RCSTQKVSFGTIVLSLSPETGRIATLSRTARSNSADGRSGDPLPSR 982  
 952 PQOQOQPQ:PRCK-QKVIFSGTIVLSLSPETGRIATLSRTARSNSADGRSGDPLPSR 1010  
 983 HHQDQPPQ:KCBOPANDARYKAAPTKGILESFGSKERP 1021  
 1011 H:-----QALLPLQCADADSEMTIOETGLQGMVGDHQP 1043

RESULT 6  
 CASR\_MOUSE  
 ID CASR\_MOUSE STANDARD; PAT: 1079 AA  
 AC Q9QY96; O08968; Q9QY95; Q9QZ08; Q9RID6; Q9R1Y2;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid  
 DE Cell calcium-sensing receptor).  
 GN Name=CaSR; Synonyms=Gprc2a;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.

RC STRAIN=C57BL/6; TISSUE=Kidney;  
 RX MEDLINE=20092890; PubMed=10625662;  
 RA Oda Y., Tu C.-L., Chang W., Crumrine D., Koemueves L., Mauro T.,  
 RA Elias P.M., Bixle D.D.;  
 RT "The calcium sensing receptor and its alternatively spliced form in  
 RT murine epidermal differentiation.";  
 RL J. Biol. Chem. 275:1183-1190(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.  
 RC STRAIN=Black Swiss X 129/SV; TISSUE=Kidney;  
 RX MEDLINE=20119279; PubMed=10652312;  
 RA Pi M., Garner S.C., Flannery P., Spurney R.F., Quarles L.D.;  
 RT "Genes of extracellular cations in CasR-deficient osteoblasts.  
 RT murine epidermal differentiation.";  
 RL J. Biol. Chem. 275:3256-3263(2000).  
 RN [3]  
 RP SEQUENCE OF 256-600 FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.  
 RC TISSUE=Epiphyseal cartilage;  
 RX MEDLINE=20043955; PubMed=10579354;  
 RA Chang W., Tu C., Chen T.-H., Komuves L., Oda Y., Pratt S.A.,  
 RA Miller S., Shoback D.;  
 RT "Expression and signal transduction of calcium-sensing receptors in  
 RT cartilage and bone.";  
 RL Endocrinology 140:5883-5893(1999).  
 RN [4]  
 RP SEQUENCE OF 507-582 FROM N.A. (ISOFORM A).  
 RC STRAIN=NMRI; TISSUE=Brain;  
 RA Hildenbrand J., Ammon H.P.T., Wahl M.A.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 562-814 FROM N.A.  
 RC TISSUE=Kidney;  
 RA Moawad T.I., Riccardi D.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 646-799 FROM N.A., AND TISSUE SPECIFICITY.  
 RX MEDLINE=97231187; PubMed=9076582;  
 RA Charles L.D., Hartle J.E. II, Siddhanti S.R., Guo R., Hinson T.K.;  
 RT "A distinct cation-sensing mechanism in MC3T3-E1 osteoblasts  
 RT functionally related to the calcium receptor.";  
 RL J. Bone Miner. Res. 12:393-402(1997).  
 CC -!- FUNCTION: Senses changes in the extracellular concentration of  
 CC calcium ions. The activity of this receptor is mediated by a G-  
 CC protein that activates a phosphatidylinositol-calcium second  
 CC messenger system.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=A;  
 CC IsoId=Q9QY96-1; Sequence=Displayed;  
 CC Name=B;  
 CC IsoId=Q9QY96-2; Sequence=VSP\_002036;  
 CC -!- TISSUE SPECIFICITY: Epidermis, kidney and cartilage.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor family 3.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 CC EMBL; AF110178; AAD28371.1; -  
 CC EMBL; AF110179; AAD28372.1; -  
 CC EMBL; AF128842; AAD40638.1; -  
 CC EMBL; AF068900; AAC19388.1; -  
 CC EMBL; AB027140; BAA77688.1; -  
 CC EMBL; AF02015; AAC53252.1; -  
 CC EMBL; AF159565; AAF00193.1; -  
 CC HSSP; P23385; LEWK.  
 CC MGD; MGI:1351351; Gprc2a.  
 CC InterPro; IPR001828; ANF\_receptor.

DR InterPro; IPR000068; Ca\_sens\_receptor.  
 DR InterPro; IPR000337; GPCR\_Mg.  
 DR Pfam; PF00003; 7tm\_3; 1. \_Mg.  
 DR Pfam; PF01094; ANF\_receptor; 1.  
 DR PRINTS; PR00248; GPCR\_Mg.  
 DR PROSITE; PS00979; G\_PROTEIN\_RECP\_F3\_1; 1.  
 DR PROSITE; PS00980; G\_PROTEIN\_RECP\_F3\_2; 1.  
 DR PROSITE; PS00981; G\_PROTEIN\_RECP\_F3\_3; 1.  
 DR PROSITE; PS00982; G\_PROTEIN\_RECP\_F3\_4; 1.  
 DR PROSITE; PS0259; G\_PROTEIN\_RECP\_F3\_4; 1.  
 KW Alternative splicing; G-protein coupled receptor; Glycoprotein;  
 KW Signal; Transmembrane.  
 FT SIGNAL 1..19 Potential.  
 FT CHAIN 20..1079 Extracellular calcium-sensing receptor.  
 FT DOMAIN 20..612 Extracellular (Potential).  
 FT TRANSMEM 613..635 1 (Potential).  
 FT DOMAIN 636..649 Cytoplasmic (Potential).  
 FT TRANSMEM 650..670 2 (Potential).  
 FT DOMAIN 671..681 Extracellular (Potential).  
 FT TRANSMEM 682..700 3 (Potential).  
 FT DOMAIN 701..724 Cytoplasmic (Potential).  
 FT TRANSMEM 725..745 4 (Potential).  
 FT DOMAIN 746..769 Extracellular (Potential).  
 FT TRANSMEM 770..792 5 (Potential).  
 FT DOMAIN 793..805 Cytoplasmic (Potential).  
 FT TRANSMEM 806..828 6 (Potential).  
 FT DOMAIN 829..836 Extracellular (Potential).  
 FT TRANSMEM 837..862 7 (Potential).  
 FT DOMAIN 863..1079 Cytoplasmic (Potential).  
 FT CARBOHYD 90..90 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 130..130 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 261..261 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 287..287 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 386..386 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 446..446 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 468..468 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 488..488 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 541..541 N-linked (GlcNAc. .) (Potential).  
 FT CARBOHYD 594..594 N-linked (GlcNAc. .) (Potential).  
 FT VARSPIC 461..537 Missing (in isoform B).  
 FT /FTIC=VSP\_002036.  
 FT A -> S (in Ref. 2).  
 FT L -> P (in Ref. 3).  
 FT G -> D (in Ref. 2 and 3).  
 FT V -> A (in Ref. 2).  
 FT Y -> H (in Ref. 2).  
 FT E -> V (in Ref. 2, 3 and 5).  
 FT F -> L (in Ref. 5).  
 FT L -> I (in Ref. 2).  
 FT TGSN -> SGWI (in Ref. 2).  
 FT V -> M (in Ref. 2).  
 FT V -> A (in Ref. 2).  
 FT I -> V (in Ref. 2).  
 SQ SEQUENCE 1079 AA; 120839 MW; AAFSD8D472736D6E CRC64;  
 Query Match 73.5%; Score 3976.5; DB 1; Length 1079;  
 Best Local Similarity 74.3%; Pred. No. 1.5e-270;  
 Matches 772; Conservative 88; Mismatches 124; Indels 55; Gaps 7;  
 QY 15 LQSVNVSNGPNOAQQKDIILGLPFIHFGVAKKDCLKSRPEATKCIYRNGFRW 74  
 DB 11 LALTWHSSAAYGPDQQAQKGGDIILGLPFIHFGVAKKDCLKSRPEATKCIYRNGFRW 70  
 QY 75 LQAMFAIEEINNSMTFLPNITLGYRIEDTNTVSKALEATLSVAQNKIDSLNLDFFCN 134  
 DB 71 LQAMFAIEEINNSMTFLPNITLGYRIEDTNTVSKALEATLSVAQNKIDSLNLDFFCN 130  
 QY 135 CSDHIPSTIANVGATSGISITAVANLLGLFPIPOVSASSRLSLNKNKAYKAFRTIPND 194  
 DB 131 CSEHIPSTIANVGATSGISITAVANLLGLFPIPOVSASSRLSLNKNKAYKAFRTIPND 190  
 QY 195 EQQATAMAEIIEHFQWNVGTLAADDYGRGIDKFREEAVKRDICIDFSEMISOYTKQ 254  
 DB 191 EQQATAMAEIIEHFQWNVGTLAADDYGRGIDKFREEAVKRDICIDFSEMISOYTKQ 250

QY 255 QLEFIADVIONSSAKVIVFSGPDLEPLTOEIVRRNITDRIWLASEAWASSSLIAKPEY 314  
 DB 251 EIQQVVEIQNSTAKVIVFSGPDLEPLTOEIVRRNITDRIWLASEAWASSSLIAKPEY 310  
 QY 315 FHVGGTIGFALRAGRIPGFNKELKEVHPSRSSDNGFVKEFWETFCYFETKTLQK- 373  
 DB 311 FHVGGTIGFALRAGRIPGFNKELKEVHPSRSSDNGFVKEFWETFCYFETKTLQK- 370  
 QY 374 NSKVPISGHPAAQGDGSAKHSRRTALRHPCTGENTISVETPYLDYTHLRISVNVVAVY 433  
 DB 371 DTFVRSH---EKGNNLLNS-STAFRPLCTGDNINSVETPYNGVEHLRISVNVVAVY 425  
 QY 434 SIAHALQDIHSCKPGTIGFANGSCADIKKVEAQVNLHLLHKLFTNSMGQVDFDQGDGL 493  
 DB 426 SIAHALQDIYTCPLPGRGLFTNGSCADIKKVEAQVNLHLLHKLFTNSMGQVDFDQGDGL 485  
 QY 494 KGNITLIINWOLSAEDSVLFHEVGNVYNAKPSDRNLNINEKKILWSGPKVVPFNSCRD 553  
 DB 486 VGNYSIINWOLSAEDSVLFHEVGNVYNAKPSDRNLNINEKKILWSGPKVVPFNSCRD 545  
 QY 554 CVPGRKGIIEGPTCCFECMACAEGFSDENDASACTKCPNDPFWNENHTSCIAKEIEY 613  
 DB 546 CQAGTRKGIIEGPTCCFECMACAEGFSDENDASACTKCPNDPFWNENHTSCIAKEIEY 605  
 QY 614 LSWTEPFGIALTIPAVLIGILITSFVLGVFKFRNTPIVKATNRELSYLLLSLCCFSS 673  
 DB 606 LSWTEPFGIALTIPAVLIGILITSFVLGVFKFRNTPIVKATNRELSYLLLSLCCFSS 665  
 QY 674 LFIIGPRDWTCLROPAGISFVLGICILVKNRVLVFEAKIPTSLHRKWGVLNLOF 733  
 DB 666 LFIIGPRDWTCLROPAGISFVLGICILVKNRVLVFEAKIPTSLHRKWGVLNLOF 725  
 QY 734 LLVFLCILVQIVTCIILWTAPSSYRNHELEDEVIFITCDEGSLMALGLIGYTCLAA 793  
 DB 726 LLVFLCTFMQIVTCIILWTAPSSYRNHELEDEVIFITCDEGSLMALGLIGYTCLAA 785  
 QY 794 ICFFAFKSKLPENNEAKFTFSMLIPIFVWISPIPAYSTYKGFVSAVEVIALASS 853  
 DB 786 ICFFAFKSKLPENNEAKFTFSMLIPIFVWISPIPAYSTYKGFVSAVEVIALASS 845  
 QY 854 FGLLGCIYFNKCYIILFKPCRNTEIEVRGTAHAFKVAARATLRSAASRKSLSLGS 913  
 DB 846 FGLLACIFFNKCYIILFKPCRNTEIEVRGTAHAFKVAARATLRSAASRKSLSLGS 905  
 QY 914 TISSPASSTCGPG-----LTWEMQ-----RCST 936  
 DB 906 TGSNPNSSISKSNSDRFPQPERKQQQPLALTQEQQQQPLTLPQOQQOQPPQPRCK- 964  
 QY 937 QKVSFGSGVTTLSPTEEGRYATLSRTARSNSADGRSGDDLPSRHHDDQGPQKCEQP 996  
 DB 965 QKVSFGSGVTTLSPTEEGRYATLSRTARSNSADGRSGDDLPSRHHDDQGPQKCEQP 996  
 QY 997 ANDARYKAAPTGTUESPG 1015  
 DB 1022 -----ADSEWTIGETG 1032  
 RESULT 7  
 ID Q6XAF1 PRELIMINARY; PRT; 941 AA.  
 AC Q6XAF1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Calcium polyvalent cation receptor 1.  
 OC Salmo salar (Atlantic salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 RN [1]\_TaxID=8030;  
 RP SEQUENCE FROM N.A.

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RC TISSUE=Kidney;
RA Nearing J.A., Harris W.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY245445; AAP79925.1; -.
DR GO: GO:0004872; P:receptor activity; IEA.
DR InterPro; IPR001828; ANF_receptor.
DR InterPro; IPR000688; Ca_sens_receptor.
DR InterPro; IPR000337; GPCR_Mgr.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASSENSINGR.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
DR KW Receptor.
SQ SEQUENCE 941 AA; 106130 MW; 06119219CDF62D1F CRC64;

Query Match 68.9%; Score 3728; DB 2; Length 941;
Best Local Similarity 74.7%; Pred. No. 3.9e-253;
Matches 711; Conservative 97; Mismatches 116; Indels 28; Gaps 6;

QY 8 LLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAADQDLKSRPEATKICRY 67
DB 8 LVLLGFSSV-----ISTYGPQRAQKGTGILLGGLFPMHFGVTSKDQDLAARPESTECVRY 63

QY 68 NFRGRFWLQAMIFAIBEINNSMTPLNITLGVRIPTDNTVSKALEATLSFVAQNKIDSL 127
DB 64 NFRGRFWLQAMIFAIBEINNSMTPLNITLGVRIPTDNTVSKALEATLSFVAQNKIDSL 123

QY 128 NLDEFNCSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSNKNEYKAF 187
DB 124 NLDEFNCSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSNKNEYKAF 183

QY 188 LRTIPNDEQQAAMAEIIEHFQWNVGTTLAADDYGRPGIDKPREAVKRDICIDFSEMI 247
DB 184 MRTIPTDEHQATAMADIIDYFQWNVIAVSDDEYGRPGIEKFEKEMEEDICIHLSLI 243

QY 248 SOYVTKQLFADVIQNSAKVIVFNSGPDLEPLIQEIVRNITDRIWLASEAWASS 307
DB 244 SQYFEWQIQLVDRIENSASKIVIVFNSGPDLEPLIQEIVRNITDRIWLASEAWASS 303

QY 308 LIAKPEYFHVVGTTIGFALRAGRIPIGNKFLKEVHPSRSSDNGFVKEFWSETNFCYTEK 367
DB 304 LIAKPEYLDVVVGTTIGFALRAGRIPIGNKFLKEVHPSRSSDNGFVKEFWSETNFCYLED 363

QY 368 TLTKLNKSVPHCPAQGDGSKAGNSRRRTALRHPTCGEENITSVETPYLDYTHLRISYN 427
DB 364 --QLRDS-----NGS-----TSFRPLCTGDEIDMGAETPYLDYTHLRISYN 404

QY 428 VYVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAWQVNLHLHLKFTNSMGEQVDF 487

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705 GLNLQFLLVFLFTFVQVMTCVWLYNAPPASYNHDI-DELIITCNEGSMALGLIGY 763
788 TCLAACFPFAFKSRKLPENFNEAKITFTSMILFPIVWISFIPAVSYGKPVSAVEVI 847
764 TCLAACFPFAFKSRKLPENFTEAKITFTSMILFPIVWISFIPAYFSTYGFVSVEVI 823
848 AILASSGGLLCIVFNKCIILFKPCRNTEEVRCSTAAHAFKVAARATLRRSAARKS 907
824 AILASSGGLLACIFFNKKVILILFKPSRNTEEVRCSTAAHAFKVAARATLRRSAARKS 883
908 SSLCGSTISSPASS---TCGPGLTMMQRCSTQKVSFGSGTVTLSLSFEET 955
884 SSVGGSCASTPSSSISLKTNDNDSPGQRIHKPRVSGSGTVTLSLSFEES 935

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RESULT 8
AAP79925
ID AAP79925 PRELIMINARY; PRT; 941 AA.
AC AAP79925;
DT 03-MAR-2004 (T-EMBLrel. 27, Created)
DT 03-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DT 03-MAR-2004 (T-EMBLrel. 27, Last annotation update)
DE Calcium polyvalent cation receptor 1.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Nearing J.A., Harris W.;
RT "Tissues of Atlantic Salmon (Salmo salar) Express Multiple Polyvalent
RT Cation Sensing Receptor (Car) cDNAs that Appear to Mediate Salinity
RT Sensing."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY245445; AAP79925.1; -.
KW Receptor.
SQ SEQUENCE 941 AA; 106130 MW; 06119219CDF62D1F CRC64;

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Query Match 68.9%; Score 3728; DB 2; Length 941;
Best Local Similarity 74.7%; Pred. No. 3.9e-253;
Matches 711; Conservative 97; Mismatches 116; Indels 28; Gaps 6;

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QY 8 LLFLGFTLLQSNVSGYGNQRAQKGGDIILGGLFPIHFGVAADQDLKSRPEATKICRY 67
DB 8 LVLLGFSSV-----ISTYGPQRAQKGTGILLGGLFPMHFGVTSKDQDLAARPESTECVRY 63

QY 68 NFRGRFWLQAMIFAIBEINNSMTPLNITLGVRIPTDNTVSKALEATLSFVAQNKIDSL 127
DB 64 NFRGRFWLQAMIFAIBEINNSMTPLNITLGVRIPTDNTVSKALEATLSFVAQNKIDSL 123

QY 128 NLDEFNCSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSNKNEYKAF 187
DB 124 NLDEFNCSDHPSTIAVVGATGSGISTAVANLLGLFYIPQVSYASSRLLSNKNEYKAF 183

QY 188 LRTIPNDEQQAAMAEIIEHFQWNVGTTLAADDYGRPGIDKPREAVKRDICIDFSEMI 247
DB 184 MRTIPTDEHQATAMADIIDYFQWNVIAVSDDEYGRPGIEKFEKEMEEDICIHLSLI 243

QY 248 SOYVTKQLFADVIQNSAKVIVFNSGPDLEPLIQEIVRNITDRIWLASEAWASS 307
DB 244 SQYFEWQIQLVDRIENSASKIVIVFNSGPDLEPLIQEIVRNITDRIWLASEAWASS 303

QY 308 LIAKPEYFHVVGTTIGFALRAGRIPIGNKFLKEVHPSRSSDNGFVKEFWSETNFCYTEK 367
DB 304 LIAKPEYLDVVVGTTIGFALRAGRIPIGNKFLKEVHPSRSSDNGFVKEFWSETNFCYLED 363

QY 368 TLTKLNKSVPHCPAQGDGSKAGNSRRRTALRHPTCGEENITSVETPYLDYTHLRISYN 427
DB 364 --QLRDS-----NGS-----TSFRPLCTGDEIDMGAETPYLDYTHLRISYN 404

QY 428 VYVAVYSIAHALQDIHSCKPGTGFANGSCADIKKVEAWQVNLHLHLKFTNSMGEQVDF 487

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Db 405 VYVAVHSIAQALQDILTCIPGRGLFNNNSCADIKKTEAMQVLLKQLRHLNFSNMGKRVHF 464  
 QY 488 DQGDGLGNVTIINWOLSAEDSVLPHVGNVNAVAKPSDRININEKKILWSGFSKVWPP 547  
 Db 465 DENADPSGNTIINWHSRSPEDSVFEEVGFYNNRAKRGVQLFIDNTKILMNGYTEVPP 524  
 QY 548 SNCRDVCPTGRKGIIEGPTCCFECMACAEFSDENDASACTKCPNDPWSNENHTSCI 607  
 Db 525 SNCSDECEPTGRKGIIESMPTCCFECTECSEGEYSDHDXASVCTKCPNDSNENHTSCF 584  
 QY 608 AXEIVLWTEPFGIALTCVGLILITSVFVTKFRNTPIVKTNRVLLVFEAKIPTSLHRKWV 727  
 Db 595 LKEIEFELWTEPFGIALCULVGLVPLTAFVNGVFIKFRNTPIVKTNRVLLVFEAKIPTSLHRKWV 704  
 QY 668 CCFSSSLIFIGBPQDWTCLRQPAFGISFVLCSILVKTNRVLLVFEAKIPTSLHRKWV 727  
 Db 645 CCFSSSLIFIGBPQDWTCLRQPAFGISFVLCSILVKTNRVLLVFEAKIPTSLHRKWV 704  
 QY 728 GLNLQFLVLCILVQIVTCIWLTPAPPSYRNHEDEVIITCDEGSLMAGFLICY 787  
 Db 705 GLNLQFLVLCILVQIVTCIWLTPAPPSYRNHEDEVIITCDEGSLMAGFLICY 787  
 QY 788 TCLLAACFFFAKSKRLPENNEAKFITFSMLIFPIVWISFIPAYSTYGFVSAVEVI 847  
 Db 764 TCLLAACFFFAKSKRLPENNEAKFITFSMLIFPIVWISFIPAYSTYGFVSAVEVI 823  
 QY 848 AILASSFGLLCIYFNKCVIILFKPCRNTEIEVRGCTAAHAFKVAARATLRSASRKRS 907  
 Db 824 AILASSFGLLCIYFNKCVIILFKPCRNTEIEVRGCTAAHAFKVAARATLRSASRKRS 883  
 QY 908 SSICGSTISSPASS---TCGPGLTNEMORCSTQKVSFGSGVTLSLSPEET 955  
 Db 884 SSVGGSCASTPSSISLKTNDNDSFGQRIHKPRVSGSGVTLSLSPEES 935

RESULT 9  
 Q6XAF3  
 ID O6XAF3 PRELIMINARY; PRT; 941 AA.  
 AC O6XAF3  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Calcium polyvalent cation receptor 2.  
 OS Salmo salar (Atlantic salmon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Proacanthopterygii; Salmoniformes; Salmonidae; Salmo.  
 OX NCBI\_TaxID=8030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Nearing J.A., Harris W.,  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY254443; AAP79923.1; -.  
 DR GO; GO:0004872; Fireceptor activity; IEA.  
 DR InterPro; IPR001828; ANF receptor.  
 DR InterPro; IPR000068; Ca\_sens receptor.  
 DR InterPro; IPR000337; GPCR Mgr.  
 DR InterPro; IPR011500; NCD3G\_GPCR.  
 DR Pfam; PF00003; 7tm\_3; 1.  
 DR Pfam; PF01094; ANF receptor; 1.  
 DR Pfam; PF07562; NCD3G; 1.  
 DR PRINTS; PRO0592; CASSENSINGR.  
 DR PRINTS; PRO0248; GPCRMR.  
 DR PROSITE; PS00979; G\_PROTEIN RECEPTOR F3; 1; 1.  
 DR PROSITE; PS50259; G\_PROTEIN RECEPTOR F3; 4; 1.  
 KW Receptor.  
 SQ SEQUENCE 941 AA; 106072 MW; C72B91C00290FF27 CRC64;  
 Query Match 68.8%; Score 3721; DB 2; Length 941;  
 Best Local Similarity 74.6%; Pred. No. 1.2e-252;  
 Matches 710; Conservative 97; Mismatches 117; Indels 28; Gaps 6;

QY 8 LLFLGFTLLQSYNVSGYGNQRAQKKGDIILGGLFPIHFGVAAKQDQDLKSRPEATKIRY 67  
 Db 8 LVLLGFSV---ISTVGPQRAQKQKDIILGGLFPMHFGVTSKQDQDLAARPESTECVRY 63  
 QY 68 NFRGFRWLQAMIFAIBEINNSMTFLPNIILGYRIFDTCTNTVSALBATISFVAQNKIDSL 127  
 Db 64 NFRGFRWLQAMIFAIBEINNSMTFLPNIILGYRIFDTCTNTVSALBATISFVAQNKIDSL 123  
 QY 128 NLDEFNCSDHIPTSTIAVGCATGISTAVANLLGLFYIPOVSYASSSLLSNKNEYKAF 187  
 Db 124 NLDEFNCSDHIPTSTIAVGCATGISTAVANLLGLFYIPOVSYASSSLLSNKNEYKAF 183  
 QY 188 LRIPNDEQOATAMAEIIEHFQNNWGTAAADDDYGRPGIDKPREBAVKRDCIDISEMI 247  
 Db 184 MRTIPTDEHOATAMADIIDYFQNNWVIAVSDDEYGRPGIEKPEKEMEERDICIHLSELI 243  
 QY 248 SOYVTKQLEFIADVLONSSAKVIVFSGNPDLEPLIQEIVRENITDRILWASEAASS 307  
 Db 244 SOYFEEWQIGLVRIENSASAKVIVFSGPDLEPLIKEMVRNITDRILWASEAASS 303  
 QY 308 LIAKPEYFHVVGTTIGFALRAGRIPGFNKFLKEVHPSRSDNGFVKEFWEEFPCYFTEK 367  
 Db 304 LIAKPEYLDVVVGTTIGFALRAGRIPGKDFQEBVTPKSSHNEFVREFWEETPCYLEDS 363  
 QY 368 TLTLKNSKVPSPGPAQGDGSKAGNSRRRTALRHPTCTGEENITSVETPYLDLTHLISYN 427  
 Db 364 --QLRDSSE-----NGS-----TSRPLCTGEEDINGAETPYLDLTHLISYN 404  
 QY 428 VYVAVVSIHALQDIHSCCKPGTGFANGSCADIKKVEAMQVLLHLKFTNSMGEOVDF 487  
 Db 405 VYVAVHSIAQALQDILTCIPGRGLFNNNSCADIKKTEAMQVLLKQLRHLNFSNMGKRVHF 464  
 QY 488 DQGDGLGNVTIINWOLSAEDSVLPHVGNVNAVAKPSDRININEKKILWSGFSKVWPP 547  
 Db 465 DENADPSGNTIINWHSRSPEDSVFEEVGFYNNRAKRGVQLFIDNTKILMNGYTEVPP 524  
 QY 548 SNCRDVCPTGRKGIIEGPTCCFECMACAEFSDENDASACTKCPNDPWSNENHTSCI 607  
 Db 525 SNCSDECEPTGRKGIIESMPTCCFECTECSEGEYSDHDXASVCTKCPNDSNENHTSCF 584  
 QY 608 AXEIVLWTEPFGIALTCVGLILITSVFVTKFRNTPIVKTNRVLLVFEAKIPTSLHRKWV 727  
 Db 585 LKEIEFELWTEPFGIALCULVGLVPLTAFVNGVFIKFRNTPIVKTNRVLLVFEAKIPTSLHRKWV 704  
 QY 668 CCFSSSLIFIGBPQDWTCLRQPAFGISFVLCSILVKTNRVLLVFEAKIPTSLHRKWV 727  
 Db 645 CCFSSSLIFIGBPQDWTCLRQPAFGISFVLCSILVKTNRVLLVFEAKIPTSLHRKWV 704  
 QY 728 GLNLQFLVLCILVQIVTCIWLTPAPPSYRNHEDEVIITCDEGSLMAGFLICY 787  
 Db 705 GLNLQFLVLCILVQIVTCIWLTPAPPSYRNHEDEVIITCDEGSLMAGFLICY 787  
 QY 788 TCLLAACFFFAKSKRLPENNEAKFITFSMLIFPIVWISFIPAYSTYGFVSAVEVI 847  
 Db 764 TCLLAACFFFAKSKRLPENNEAKFITFSMLIFPIVWISFIPAYSTYGFVSAVEVI 823  
 QY 848 AILASSFGLLCIYFNKCVIILFKPCRNTEIEVRGCTAAHAFKVAARATLRSASRKRS 907  
 Db 824 AILASSFGLLCIYFNKCVIILFKPCRNTEIEVRGCTAAHAFKVAARATLRSASRKRS 883  
 QY 908 SSICGSTISSPASS---TCGPGLTNEMORCSTQKVSFGSGVTLSLSPEET 955  
 Db 884 SSVGGSCASTPSSISLKTNDNDSFGQRIHKPRVSGSGVTLSLSPEES 935

RESULT 10  
 AAP79923  
 ID AAP79923 PRELIMINARY; PRT; 941 AA.  
 AC AAP79923;  
 DT 03-MAR-2004 (T-EMBLrel. 27, Created)  
 DT 03-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 03-MAR-2004 (T-EMBLrel. 27, Last annotation update)





184 MRTIPTDEYQATAMADIIIBFFQWNVYASVADDDYGRPGVEXFEKEMEERDICIHLNELI 243  
 248 SOYVYKQLEFADVTIONSAKVIIVFSGNPDLEPLIOEIVERNITDRIWLASEAWASS 307  
 244 SQFDEHEIQALADRIENSTAKVIIVFSGNPDLEPLIOEIVERNITDRIWLASEAWSSS 303  
 308 LIAKPYFHVVGTTIGFALRAGRIPOGKFLKEVHPSRSSDNGFVKEFEETFCYFEK 367  
 304 LIAKPYLDVAGTTIGFALRAGRIPOGKFLKEVHPSRSSDNGFVKEFEETFCYFEK 363  
 368 TITQKNSKVPBGHGAQDGSAGNSRRTALRHCTGEENITSVETPYLDYTHLRISYN 427  
 364 --PRQOSE-----NGS-----TSRPLCTGEEDITSVETPYLDYTHLRISYN 404  
 428 VYVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAWQVNLHLHLKFTNSMGEOVDF 487  
 405 VYVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAWQVNLHLHLKFTNSMGEOVDF 464  
 488 DOGDLKGNYYTINWLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILMSGFGKVPVP 547  
 465 DENADLAANYTILNWHRSADGSVVFEEVGYVYHMAKRGKLFIDNTKILMNGFSSEVPF 524  
 548 SNCSRDVPGTRKGIIEGPTCCFECMACAEFSDENDASACTCPNDPWSNENHTSCI 607  
 525 SNCSDECEGTRKGIIEGPTCCFECMACAEFSDENDASACTCPNDPWSNENHTCF 584  
 608 AXEIEYLSWTEPFGIALTIFAVLGILITSVLGVIKFRNTPIVKATNRELSYLLFSLI 667  
 585 LKEIEFLSWTEPFGIALTIFAVLGILITSVLGVIKFRNTPIVKATNRELSYLLFSLI 644  
 668 CFFSSLIIFIGQDMWMLRQAPAGISFVLGICILVKTNRVLVFAKIPTSILHRKW 727  
 645 CFFSSLIIFIGQDMWMLRQAPAGISFVLGICILVKTNRVLVFAKIPTSILHRKW 704  
 728 GLNQLPFLVLCILVQIVTCIIWLTAPPSSYRNHELEDEVIFITCDEGSLMALGFLIGY 787  
 705 GLNQLPFLVLCILVQIVTCIIWLTAPPSSYRNHELEDEVIFITCDEGSLMALGFLIGY 763  
 788 TCLAACIFFAFKSKRLBENFEAKFITFSMLIFIVWISFIPAYVSTYKFSVAEVI 847  
 764 TCLAACIFFAFKSKRLBENFEAKFITFSMLIFIVWISFIPAYVSTYKFSVAEVI 823  
 848 AILASSFGLGICITFNKCVIILFKPCRNTEBVRCTAAHAFKVAARATLRSASRKS 907  
 824 AILASSFGLGICITFNKCVIILFKPCRNTEBVRCTAAHAFKVAARATLRSASRKS 883  
 908 SSLCGSTISSPASSTCGPGLTWEMQRCST-----QKVSFGSGTWTLSLSFEETR 957  
 884 SSIGSSSTPSSSI---SLKTNMGDCATSGKRPVSGSGTWTLSLSFEETR 936

RESULT 12

073635 PRELIMINARY; PRT; 940 AA.  
 AC 073635;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Calcium2+ sensing receptor  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98226788; PubMed=9560249;  
 RA Naito T., Saito Y., Yamamoto J., Nozaki Y., Tomura K., Hazama M.,  
 RA Nakanishi S., Brenner S.;  
 RT "Putative pheromone receptors related to the Ca2+-sensing receptor in  
 RT Fugu.";

Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).  
 RL EMBL; AB008857; BAA26122.1; -.  
 DR HSP; P23385; IEMT.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR001828; ANF\_receptor.  
 DR InterPro; IPR000068; Ca\_sens\_receptor.  
 DR InterPro; IPR000337; GPCR Mgr.  
 DR InterPro; IPR011500; NCD3G\_GPCR.  
 DR Pfam; PF00003; 7tm\_3; 1.  
 DR Pfam; PF01094; ANF\_receptor; 1.  
 DR Pfam; PF07582; NCD3G; 1.  
 DR PRINTS; PRO0592; CASENSINGR.  
 DR PRINTS; PRO0248; GPCRNGR.  
 DR PROSITE; PS00979; G\_PROTEIN\_RECEP\_F3\_1; 1.  
 DR PROSITE; PS02659; G\_PROTEIN\_RECEP\_F3\_4; 1.  
 KW Receptor.  
 SQ SEQUENCE. 940 AA; 105813 MW; 06DAB7803B6878B3 CRC64;  
 Query Match 67.4%; Score 3644.5; DB 2; Length 940;  
 Best Local Similarity 71.6%; Pred. No. 2.9e-247;  
 Matches 687; Conservative 114; Mismatches 124; Indels 35; Gaps 9;  
 QY 4 LHCOLLFLGFTLLQSYNVSGYGNQRAOKKGDIIILGGLPFIHFGVAAKQDCLKSRPEATK 63  
 DB 6 LH-YLILG-----SGVISTYGNQRAQMTGDIILGGLPFIHFGISKKDENLAARPESTK 60  
 QY 64 CIRYNGFERFLQAMIFAIIEINNSMTFLNITLGYRIEDTNTVSKALEATLSFVAQNK 123  
 DB 61 CVRFNFRGFWLQAMVFAIEEINNSSLLPNITLGYRIEDTNTVSKALEATLSFVAQNK 120  
 QY 124 IDSINLDFCNSDHPSTIAVVGATSGISITAVANLLGLFYIPOVSYASSRLLSNKE 183  
 DB 121 IDSINLDFCNCDDHPATIAVVGAGSAVSTAVANLLSLFYIPOVSYASSRLLSNKKQ 180  
 QY 184 YKAFLLTIPNDEQOATAMAEIIEHFQWNVGTLAADDYGRPGIDKFRFEAVKRDICIDF 243  
 DB 181 YKSFMTIPTDEHQATAMADVIEYFQWNVVAVASDDYGRPGIEKFEKEMEERDICIHL 240  
 QY 244 SEMISQYVYKQLEFADVTIONSAKVIIVFSGNPDLEPLIOEIVERNITDRIWLASEAW 303  
 DB 241 NELISQYFDECEITKALVDRIENSTAKVIIVFSGNPDLEPLIOEIVERNITDRIWLASEAW 300  
 QY 304 ASSSLIAKPYFHVVGTTIGFALRAGRIPOGKFLKEVHPSRSSDNGFVKEFEETFCY 363  
 DB 301 ASSSLIAKPYLDVAGTTIGFALRAGRIPOGKFLKEVHPSRSSDNGFVKEFEETFCY 360  
 QY 364 FTEKTLTQKNSKVPBGHGAQDGSAGNSRRTALRHCTGEENITSVETPYLDYTHLR 423  
 DB 361 LEDSS--PRQOSE-----NGS-----DSRPLCTGEEDITSVETPYLDYTHLR 401  
 QY 424 ISYNVVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAWQVNLHLHLKFTNSMGE 483  
 DB 402 ISYNVVAVYSIAHALQDIHSCPKGTGIFANGSCADIKKVEAWQVNLHLHLKFTNSMGE 461  
 QY 484 QVDFDQDGLKGNYYTINWLSAEDSVLFHEVGNYNAYAKPSDRNLNINEKILMSGFGK 543  
 DB 462 KVHFDENADMEANYTIINWHRSADGSVVFEEVGYVYHMAKRGKLLIDNTKMMNAYSS 521  
 QY 544 VVFPNSCRDVCVPTKGIIEGPTCCFECMACAEFSDENDASACTCPNDPWSNENH 603  
 DB 522 EVFPNSCEDCEGTRKGIIEGPTCCFECMACAEFSDENDASACTCPNDPWSNENH 581  
 QY 604 TSICAKIEYLSWTEPFGIALTIFAVLGILITSVLGVIKFRNTPIVKATNRELSYLL 663  
 DB 582 TFCFLKEIEFLSWTEPFGIALTIFAVLGILITSVLGVIKFRNTPIVKATNRELSYLL 641  
 QY 664 FSLIICFSSSLIFIGQDMWMLRQAPAGISFVLGICILVKTNRVLVFAKIPTSILHR 723  
 DB 642 LSLIICFSSSLIFIGQDMWMLRQAPAGISFVLGICILVKTNRVLVFAKIPTSILHR 701  
 QY 724 RKWVGLNQLPFLVLCILVQIVTCIIWLTAPPSSYRNHELEDEVIFITCDEGSLMALGF 783

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Db 702 RQWGLNQLVFLVCTFQVNMICVWLYNAPSSRYNNDI-DEIFITCNEGSMALGF 760
Qy 784 LIGYCLLAACIACFFAFKSRKLPENFNKAFITFSLNLIFFIWIWISFIPAYSTYCKFYSA 843
Db 761 LIGYCLLAACIACFFAFKSRKLPENFNKAFITFSLNLIFFIWIWISFIPAYSTYCKFYSA 820
Qy 844 VEVIAILASSFGLGCIYFNKCYIILFKPCRNTEIEVRCSTAAHAFKVAARATLRRSAAS 903
Db 821 VEVIAILASSYGLACIIFNKKVYIILFKPCRNTEIEVRCSTAAHAFKVAARATLKHRTTV 880
Qy 904 RKRSSLCGSTSSPASSCGGLTWEMQRCST-----QKVSFGSGTWTLSLSPTEETR 957
Db 881 RKKSNSI-GSTASTPSSSI---SLKNSNDCDSASGRHRPRVSGGTWLSLSPESRR 936

RESULT 13
Q6XAF2
ID Q6XAF2 PRELIMINARY; PRT; 850 AA.
AC Q6XAF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Calcium polyvalent cation receptor 3.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Nearing J.A., Harris W.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY245444; AAF79924.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR001828; ANF receptor.
DR InterPro; IPR000068; Ca_sens receptor.
DR InterPro; IPR000337; GPCR_Mg2.
DR InterPro; IPR011500; NCD3G_GPCR.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF receptor; 1.
DR Pfam; PF07562; NCD3G; 1.
DR PRINTS; PR00592; CASSENSINGR.
DR PRINTS; PR00248; GPCRMR.
DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
DR PROSITE; PS00259; G_PROTEIN_RECEP_F3_4; 1.
DR Receptor.
KW Receptor.
SQ SEQUENCE 850 AA; 96544 MW; 7E2B785FED3081B9 CRC64;

Query Match 63.9%; Score 3456; DB 2; Length 850;
Best Local Similarity 75.5%; Pred. No. 4.6e-234;
Matches 650; Conservative 88; Mismatches 99; Indels 24; Gaps 5;

Qy 8 LLFLGFTLLQSNVSGYGNQRAQKGDIIILGGLPPIHFGVAAKQDOLKSRPEATKCIY 67
Db 8 LVILGFPSSV---ISTYGPQRAQKTGDIILGGLPPIHFGVTSKDQDLAARPESTECVRY 63

Qy 68 NERGFELQAMIFATEIENNSMTFLPNITLGYRIEDTNTVSKALEATLSFVAQNKIDSL 127
Db 64 NERGFELQAMIFATEIENNSMTFLPNITLGYRIEDTNTVSKALEATLSFVAQNKIDSL 123

Qy 128 NLDFEFCNCDHIPSTIAVVGATGSGISTAVANLLGLFIYIPQVSYASSRLLSNKNEYKAF 187
Db 124 NLDFEFCNCDHIPSTIAVVGASSAVSTAVANLLGLFIYIPQISYASSRLLSNKQPKSF 183

Qy 188 LTIPIDEQOATAMAEIIEHFQNWVGTAAADDDYGRPGIDKPREAVKRDICIDPSEMI 247
Db 184 MRETIPTDEQATAMADIIDYFQNWVIAVASDDEYGRPGIEKFEKEMBERDICIHLSELI 243

Qy 248 SOYVYTKQLEFTADVTONSSAKVIVVFSNGPDLPLEIQEIVRNITDRIWLASEAWSSS 307
Db 244 SOYFPEWQIQGLVDRIENSSAKVIVVFSNGPDLPLEIKEMVRNITDRIWLASEAWATS 303

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Qy 308 LIAKPEYFHVVGTTIGFALRAGIPQGNKFLKPVHPSRSSDGNFVKFWEETNCYPTK 367
Db 304 LIAKPEYLDVVGTTIGFALRAGIPQGNKFLKPVHPSRSSDGNFVKFWEETNCYLED 363
Qy 368 TLQCLNSKVPSCHPAAQGDGSKAGNSRRRTALRHPTCGENITSVETPYLDYTHLRSYN 427
Db 364 --QLRDRSE-----NGS-----TSFRPLCTGEEDIMGAETPYLDYTHLRSYN 404
Qy 428 VYVAVYSIAHALDIIHSCKPGTGFIFANGSCADIKKVEAMQVNLHLHLKFTNSMGQVDF 487
Db 405 VYVAVHSIAQALQDILTCIFGRGFFSNNSCADIKKIEAMQVLAHLNFSNSMGKVFH 464
Qy 488 DDQDLKGNVTIINWQLSADESVLPHEVGNVYAYAKPSDRNLNINEKKILWSGFSKVVPF 547
Db 465 DENADPSGNTYIINWHRSPEDGSVWFEEVGFYNNRAKRGVQLFDINTKILWNYNTEVPF 524
Qy 548 SNCRDCVPGTRXGIIBGEPTCCFECMACAEGFSDENDASACTKCPNDFWSNENHTSCI 607
Db 525 SNCSDECEPGRXGIIBSMFTCCFECTECSEGYSHKDAVCTKCPNDSWSNENHTSCF 584
Qy 608 AKIEYLSWTEPFGIALTIPAVILGILITSFVLGVFKFRNTPVVKATNRELSYLLFSLI 667
Db 585 LKIEIFLSWTEPFGIALGCVLGVLTAFVGVFKFRNTPVVKATNRELSYLLFSLI 644
Qy 668 CCFSSSIIFIGEPBDWTCRLRQPAFGISFVLCISLIVKTNRLVLYVFEAKIPTSLHRKW 727
Db 645 CCFSSSIIFIGEPQDWTCLRQPAFGISFVLCISLIVKTNRLVLYVFEAKIPTSLHRKW 704
Qy 728 GLNLQFLVFLCILVQIVTCTIIMLYTAPSSSYRNHELEDEVIIFITCDGSLMALGFLIGY 787
Db 705 GLNLQFLVFLFTFVQVMI CVWMLYNAPPASYNHDI-DBIIITCNEGSMALGFLIGY 763
Qy 788 TCLLAACIFFFAPKSRKLPENFNKAFITFSLNLIFFIWIWISFIPAYSTYCKFYSAVEVI 847
Db 764 TCLLAACIFFFAPKSRKLPENFNKAFITFSLNLIFFIWIWISFIPAYSTYCKFYSAVEVI 823
Qy 848 AILASSFGLGCIYFNKCYII 868
Db 824 AILASSFGLLACIFFNKVYII 844

RESULT 14
AAF79924
ID AAF79924 PRELIMINARY; PRT; 850 AA.
AC AAF79924;
DT 03-MAR-2004 (TrEMBLrel. 27, Created)
DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Calcium polyvalent cation receptor 3.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Nearing J.A., Harris W.;
RT "Tissues of Atlantic salmon (Salmo salar) Express Multiple Polyvalent Cation Sensing Receptor (CaR) cDNAs that Appear to Mediate Salinity Sensing.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY245444; AAF79924.1; -.
KW Receptor.
SQ SEQUENCE 850 AA; 96544 MW; 7E2B785FED3081B9 CRC64;

Query Match 63.9%; Score 3456; DB 2; Length 850;
Best Local Similarity 75.5%; Pred. No. 4.6e-234;
Matches 650; Conservative 88; Mismatches 99; Indels 24; Gaps 5;

Qy 8 LLFLGFTLLQSNVSGYGNQRAQKGDIIILGGLPPIHFGVAAKQDOLKSRPEATKCIY 67
Db 8 LVILGFPSSV---ISTYGPQRAQKTGDIILGGLPPIHFGVTSKDQDLAARPESTECVRY 63

Qy 68 NERGFELQAMIFATEIENNSMTFLPNITLGYRIEDTNTVSKALEATLSFVAQNKIDSL 127
Db 64 NERGFELQAMIFATEIENNSMTFLPNITLGYRIEDTNTVSKALEATLSFVAQNKIDSL 123

Qy 128 NLDFEFCNCDHIPSTIAVVGATGSGISTAVANLLGLFIYIPQVSYASSRLLSNKNEYKAF 187
Db 124 NLDFEFCNCDHIPSTIAVVGASSAVSTAVANLLGLFIYIPQISYASSRLLSNKQPKSF 183

Qy 188 LTIPIDEQOATAMAEIIEHFQNWVGTAAADDDYGRPGIDKPREAVKRDICIDPSEMI 247
Db 184 MRETIPTDEQATAMADIIDYFQNWVIAVASDDEYGRPGIEKFEKEMBERDICIHLSELI 243

Qy 248 SOYVYTKQLEFTADVTONSSAKVIVVFSNGPDLPLEIQEIVRNITDRIWLASEAWSSS 307
Db 244 SOYFPEWQIQGLVDRIENSSAKVIVVFSNGPDLPLEIKEMVRNITDRIWLASEAWATS 303

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Db      8  LVLGFSV-----ISTYGPQRAQKTGDILLGLFPMHFGVTSKQODLAARPESTECVRY 63
QY      68  NFRGFRWLOAMFAIBEINNSMTFLPNITLGYRIFDTCTNTVSKALEATLFSVAQNKIDSL 127
Db      64  NFRGFRWLOAMFAIBEINNSMTFLPNITLGYRIFDTCTNTVSKALEATLFSVAQNKIDSL 123
QY      128  NLDFPCNCSHDPSTIAVAGTSGISTAVANLLGLFYIPQVSYASSRLLSNKNEYKAF 187
Db      124  NLDFPCNCSHDPSTIAVAGTSGISTAVANLLGLFYIPQVSYASSRLLSNKNEYKAF 183
QY      188  LRTIPNDEOQATAMABIIHFWNWNVTGTLAADDVGRPGIDKFRPEAVKRDICIDFSMI 247
Db      184  MRTIPTDEHQATAMADIIDYFQNWVIAVASDDEVGRPGIEKFEKEMERDICIHLSELI 243
QY      248  SQYITQKLEFIADVTIONSSAKVIVVFSNGPDLPLQIPIQIIVERNITDRIWLASEAWASS 307
Db      244  SQYFEWQIQLVDRIENSSAKVIVVFSNGPDLPLQIPIQIIVERNITDRIWLASEAWASS 303
QY      308  LIAKPEYFHVVGTTGIFALRAGRIPGFNKFLXEVHPSRSSDNGFVKFEWEETFCYFTEK 367
Db      304  LIAKPEYLDVVGTGIFALRAGEIPGFKDQEVTPKXSHNEFVREFWEETFCYLED 363
QY      368  TITQLNKNVPFSGPAQOQGGKAGNSRRRTALRHFTCTGEENITSVETPYDYLRLISYN 427
Db      364  --QRLRDSB-----NGS-----TSRPLCTGEEDIMGAETPYDYLRLISYN 404
QY      428  VYVAVYSIAHALQDHSCKPGTGIFANGSCADIKKVEAKVNLHLHLKFTNSMGEQVDF 487
Db      405  VYVAVHSIAQAQDILTCIPGRGFFSNNSCADIKKIEAWQVLKQJRHNLNFSMGEKHF 464
QY      488  DQGLDKGNVTIINWLSADESVLPHEVGNVNAKPSDRININEKILMSGSKVWVF 547
Db      465  DENADPSGNTIINWHSRSPDGSVVEEVGFYNNRAKGVQLPIDNTKILNNGYNTVEPP 524
QY      548  SNGSRDVCPTGRKGIIEGPTCCFECMACAGEFSDENDASACTKPNDFNSNENHTSCI 607
Db      525  SNGSCEPCTGRKGIIESMPTCCFECTEGSEGYSDHKDASVCTKPNDSWSNENHTSCF 584
QY      608  AKIEYLSWTEPGIALTIFAVLGILITFVLGVFKPNTPIVATNRRELSYLLLSLI 667
Db      585  LKEIEFELSWTEPGIALCULGVLFATFVGVFKPNTPIVATNRRELSYLLLSLI 644
QY      668  CCFSSSLIFIGPRDWTCLRQPAFGISFVLCSICILVKTNRVLLVFAKPTSLHRKWV 727
Db      645  CCFSSSLIFIGPRDWTCLRQPAFGISFVLCSICILVKTNRVLLVFAKPTSLHRKWV 704
QY      728  GLNLQFLVLCILVQIVTCITWLYTAPPSSYRNEHEDEVIFITCDGSLMALGFLICY 787
Db      705  GLNLQFLVLCILVQIVTCITWLYTAPPSSYRNEHEDEVIFITCDGSLMALGFLICY 763
QY      788  TCLLAACFFFAFKSKPLNFENAKFIITFMSMLIFPIVWISIPAYVSTYGFVSAVEVI 847
Db      764  TCLLAACFFFAFKSKPLNFENAKFIITFMSMLIFPIVWISIPAYVSTYGFVSAVEVI 823
QY      848  AILASSFGLGCIYFNKCVII 868
Db      824  AILASSFGLGCIYFNKCVII 844

RESULT 15
Q8CDP3  PRELIMINARY; PRT; 783 AA.
AC      Q8CDP3
DT      01-MAR-2003 (TrEMBLrel. 23, Created)
DT      01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE      library, clone:4930542i18 product:calcium-sensing receptor, full
DE      insert sequence. (fragment).
GN      Name=Gprc2a;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RX      MEDLINE=99279253; PubMed=10349636;
RA      Carninci P., Hayashizaki Y.;
RT      "High-efficiency full-length cDNA cloning.";
RL      Meth. Enzymol. 303:19-44(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RX      MEDLINE=21085660; PubMed=11217851;
RA      RIKEN FANTOM Consortium;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RA      The FANTOM Consortium.
RT      The RIKEN Genome Exploration Research Group Phase I & II Team;
RT      "Analysis of the mouse transcriptome based on functional annotation of
        60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RX      MEDLINE=20499374; PubMed=11042159;
RA      Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA      Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT      "Normalization and subtraction of cap-trapper-selected cDNAs to
        prepare full-length cDNA libraries for rapid discovery of new genes.";
RL      Genome Res. 10:1617-1630(2000).
RN      [5]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RX      MEDLINE=20530913; PubMed=11076861;
RA      Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA      Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA      Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Hatada A.,
RA      Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA      Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA      Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA      Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT      "RIKEN integrated sequence analysis (RISA) system-384-format
        sequencing pipeline with 384 multicapillary sequencer.";
RL      Genome Res. 10:1757-1771(2000).
RN      [6]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6J; TISSUE=Testis;
RA      Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA      Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA      Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA      Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA      Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA      Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA      Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA      Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA      Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA      Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA      Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AK029770; BAC26608.1; -.
DR      MGD; MGII13151; Gprc2a.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0008067; F:metabotropic glutamate, GABA-B-like recepto. .; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      InterPro; IPR001828; ANF receptor.
DR      InterPro; IPR000068; Ca sens receptor.
DR      InterPro; IPR000337; GPCR_Mgr.
DR      InterPro; IPR011500; NCD3G_GPCR.
DR      Pfam; PF00003; 7tm_3; 1.
DR      Pfam; PF01094; ANF receptor; 1.
DR      Pfam; PF07562; NCD3G; 1.
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DR PRINTS; PRO0592; CASENSINGR.  
DR PRINTS; PRO0248; GPCRMRG.  
DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; 1.  
DR PROSITE; PS00981; G\_PROTEIN\_RECEP\_F3\_3; 1.  
DR PROSITE; PS00982; G\_PROTEIN\_RECEP\_F3\_4; 1.  
KW Receptor.  
FT NON\_TER  
SQ SEQUENCE 783 AA; 87795 MW; 64BAE914566E19D5 CRC64;  
  
Query Match 50.0%; Score 2707.5; DB 2; Length 783;  
Best Local Similarity 70.8%; Pred. No. 1.9e-181;  
Matches 533; Conservative 56; Mismatches 109; Indels 55; Gaps 7;  
  
QY 301 EAWASSLIAPKPEYHVVGGTIGTGFALRAGRIPGPNKFLKEVHPSRSSDNGFVKFEWETP 360  
DB 1 EAWASSLIAPKPEYHVVGGTIGTGFALRAGRIPGPNKFLKEVHPSRSSDNGFVKFEWETP 60  
  
QY 361 NCYFTEKTLTQLK-NSKVPSHGFAQGDGSKAGNSRRALTARHPCCTGGEENITSVETPYLDY 419  
DB 61 NCYFTEKTLTQLK-NSKVPSHGFAQGDGSKAGNSRRALTARHPCCTGGEENITSVETPYLDY 115  
  
QY 420 THLRISYNYVAVYSIAHALQDIHSCPGTGFANGSCADIKKVEAWQVLNHLHLKFTN 479  
DB 116 EHLRISYNYVAVYSIAHALQDIHSCPGTGFANGSCADIKKVEAWQVLNHLHLKFTN 175  
  
QY 480 SMGEQVDFDDQDGLKGYTIINWQISAEDSVLFHEVGNVAYAKPSDRININEKKILWS 539  
DB 176 NMGEQVDFDDQDGLKGYTIINWQISAEDSVLFHEVGNVAYAKPSDRININEKKILWS 235  
  
QY 540 GFSKVVPFNSCSDVCPGTRKGIIEGEPTCCPECNACAEGFSDENDASACTKCPDFFWS 599  
DB 236 GFSKVVPFNSCSDVCPGTRKGIIEGEPTCCPECNACAEGFSDENDASACTKCPDFFWS 295  
  
QY 600 NENHTSCIATKEIYLSWTEPPGIALTIFAVLGILITSVFVGFIFKFRNTPIVKATNRELS 659  
DB 296 NENHTSCIATKEIYLSWTEPPGIALTIFAVLGILITSVFVGFIFKFRNTPIVKATNRELS 355  
  
QY 660 YLLFSLICCFSSLIIFIGEPDWTCLRQAPAGISFVLCISILVKTNRVLLVFEAKIP 719  
DB 356 YLLFSLICCFSSLIIFIGEPDWTCLRQAPAGISFVLCISILVKTNRVLLVFEAKIP 415  
  
QY 720 TSLHRKWGLNLQFLVFLCILVQIVTCIIMLYTAPPSSYRNHELEDEVIFITCDGSLM 779  
DB 416 TSLHRKWGLNLQFLVFLCILVQIVTCIIMLYTAPPSSYRNHELEDEVIFITCDGSLM 475  
  
QY 780 ALGFLIGYTCILAAICFFPAKSKRLPENFNEAKITPSMLIFFIWIWISFIPAYVSTYK 839  
DB 476 ALGFLIGYTCILAAICFFPAKSKRLPENFNEAKITPSMLIFFIWIWISFIPAYVSTYK 535  
  
QY 840 FVSAREVIALASSFGLLCIYFNKCYIILPKPCRNTEEVRCSTAAHAFKVAARATLRR 899  
DB 536 FVSAREVIALASSFGLLCIYFNKCYIILPKPCRNTEEVRCSTAAHAFKVAARATLRR 595  
  
QY 900 SAASRRSSSLCGSTISSPASSTCGPG-----LTME 930  
DB 596 SAASRRSSSLCGSTISSPASSTCGPG-----LTME 655  
  
QY 931 MO-----RSTOKVSGGTVLSLSEFTGRVATLSRTARSNSADGRSGDDLPSSR 982  
DB 656 MO-----RSTOKVSGGTVLSLSEFTGRVATLSRTARSNSADGRSGDDLPSSR 714  
  
QY 983 HHDQGPQKCEFPQANDARYKAAPTKGTLESFG 1015  
DB 715 HHDQGPQKCEFPQANDARYKAAPTKGTLESFG 736

Search completed: November 17, 2004, 11:57:23  
Job time : 435 secs

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